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 Gerritsen, Mary E.
 Goddard, Audrey
 Godowski, Paul J.
 Grimaldi, J. Christopher
 Gurney, Austin L.
 Hillan, Kenneth J
 Kljavin, Ivar J.
 Kuo, Sophia S.
 Napier, Mary A.
 Pan, James;
 Paoni, Nicholas F.
 Roy, Margaret Ann
 Shelton, David L.
 Stewart, Timothy A.
 Tumas, Daniel
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Met	Val	Lys	Phe	Pro	Ala	Leu	Thr	His	Tyr	Trp	Pro	Leu	Ile	Arg
1				5					10					15

Phe	Leu	Val	Pro	Leu	Gly	Ile	Thr	Asn	Ile	Ala	Ile	Asp	Phe	Gly
				20					25					30

Glu	Gln	Ala	Leu	Asn	Arg	Gly	Ile	Ala	Ala	Val	Lys	Glu	Asp	Ala
				35				40						45

Val	Glu	Met	Leu	Ala	Ser	Tyr	Gly	Leu	Ala	Tyr	Ser	Leu	Met	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

				50					55					60				
Phe	Phe	Thr	Gly	Pro 65	Met	Ser	Asp	Phe	Lys 70	Asn	Val	Gly	Leu	Val 75				
Phe	Val	Asn	Ser	Lys 80	Arg	Asp	Arg	Thr	Lys 85	Ala	Val	Leu	Cys	Met 90				
Val	Val	Ala	Gly	Ala 95	Ile	Ala	Ala	Val	Phe 100	His	Thr	Leu	Ile	Ala 105				
Tyr	Ser	Asp	Leu	Gly 110	Tyr	Tyr	Ile	Ile	Asn 115	Lys	Leu	His	His	Val 120				
Asp	Glu	Ser	Val	Gly 125	Ser	Lys	Thr	Arg	Arg 130	Ala	Phe	Leu	Tyr	Leu 135				
Ala	Ala	Phe	Pro	Phe 140	Met	Asp	Ala	Met	Ala 145	Trp	Thr	His	Ala	Gly 150				
Ile	Leu	Leu	Lys	His 155	Lys	Tyr	Ser	Phe	Leu 160	Val	Gly	Cys	Ala	Ser 165				
Ile	Ser	Asp	Val	Ile 170	Ala	Gln	Val	Val	Phe 175	Val	Ala	Ile	Leu	Leu 180				
His	Ser	His	Leu	Glu 185	Cys	Arg	Glu	Pro	Leu 190	Leu	Ile	Pro	Ile	Leu 195				
Ser	Leu	Tyr	Met	Gly 200	Ala	Leu	Val	Arg	Cys 205	Thr	Thr	Leu	Cys	Leu 210				
Gly	Tyr	Tyr	Lys	Asn 215	Ile	His	Asp	Ile	Ile 220	Pro	Asp	Arg	Ser	Gly 225				
Pro	Glu	Leu	Gly	Gly 230	Asp	Ala	Thr	Ile	Arg 235	Lys	Met	Leu	Ser	Phe 240				
Trp	Trp	Pro	Leu	Ala 245	Leu	Ile	Leu	Ala	Thr 250	Gln	Arg	Ile	Ser	Arg 255				
Pro	Ile	Val	Asn	Leu 260	Phe	Val	Ser	Arg	Asp 265	Leu	Gly	Gly	Ser	Ser 270				
Ala	Ala	Thr	Glu	Ala 275	Val	Ala	Ile	Leu	Thr 280	Ala	Thr	Tyr	Pro	Val 285				
Gly	His	Met	Pro	Tyr 290	Gly	Trp	Leu	Thr	Glu 295	Ile	Arg	Ala	Val	Tyr 300				
Pro	Ala	Phe	Asp	Lys 305	Asn	Asn	Pro	Ser	Asn 310	Lys	Leu	Val	Ser	Thr 315				
Ser	Asn	Thr	Val	Thr 320	Ala	Ala	His	Ile	Lys 325	Lys	Phe	Thr	Phe	Val 330				
Cys	Met	Ala	Leu	Ser 335	Leu	Thr	Leu	Cys	Phe 340	Val	Met	Phe	Trp	Thr 345				

Pro	Asn	Val	Ser	Glu	Lys	Ile	Leu	Ile	Asp	Ile	Ile	Gly	Val	Asp
				350					355					360
Phe	Ala	Phe	Ala	Glu	Leu	Cys	Val	Val	Pro	Leu	Arg	Ile	Phe	Ser
				365					370					375
Phe	Phe	Pro	Val	Pro	Val	Thr	Val	Arg	Ala	His	Leu	Thr	Gly	Trp
				380					385					390
Leu	Met	Thr	Leu	Lys	Lys	Thr	Phe	Val	Leu	Ala	Pro	Ser	Ser	Val
				395					400					405
Leu	Arg	Ile	Ile	Val	Leu	Ile	Ala	Ser	Leu	Val	Val	Leu	Pro	Tyr
				410					415					420
Leu	Gly	Val	His	Gly	Ala	Thr	Leu	Gly	Val	Gly	Ser	Leu	Leu	Ala
				425					430					435
Gly	Phe	Val	Gly	Glu	Ser	Thr	Met	Val	Ala	Ile	Ala	Ala	Cys	Tyr
				440					445					450
Val	Tyr	Arg	Lys	Gln	Lys	Lys	Lys	Met	Glu	Asn	Glu	Ser	Ala	Thr
				455					460					465
Glu	Gly	Glu	Asp	Ser	Ala	Met	Thr	Asp	Met	Pro	Pro	Thr	Glu	Glu
				470					475					480
Val	Thr	Asp	Ile	Val	Glu	Met	Arg	Glu	Glu	Asn	Glu			
				485					490					

<210> 8
 <211> 535
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 33, 66, 96, 387
 <223> unknown base

<400> 8
 cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50
 tgagcttctg gtgcnttttg gctctaattc tggccacaca gagaancagt 100
 cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
 agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200
 tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttogac 250
 aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300
 ggccacatc aagaagttca ctttcgtctg catggctctg tcaactcacgc 350
 tctgtttcgt gatgttttgg acaccaacg tgtctngaa aatcttgata 400
 gacatcatcg gactggactt tgcctttgca gaactctgtg ttgttccttt 450

gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcatctca 500

ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9

<211> 434

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361

<223> unknown base

<400> 9

tgacggaatc ccgggctggg tctcctggtt tngacaagat aaacccccag 50

caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100

agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150

gttttggaca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200

tggantttgc ctttgcagaa ntttgngntg ttcttttgcg gattttctcc 250

tttttcccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350

ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400

gcgaccctgg gcggtgggttc cctcctggcg ggca 434

<210> 10

<211> 154

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 33, 49, 68, 83, 90, 98, 119

<223> unknown base

<400> 10

tattcccagt tccggtcacg gggagggcgc atntcaccgg gtggctgang 50

acactgaaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100

cgctctcacc gccagcctng tggctctacc ctacctgggg gtgcacggtg 150

agac 154

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

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<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gctctgtcac tcacgctc 18

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcatctcttc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttccgcca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<400> 16
gcctgctgtg gtcacaggtc tccg 24

<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 18
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gcctgcctgg gagcctgctc cctgctcagc tgcgcgtcct gcctctgcgg 100
ctctgcccc tgcatactgt gcagctgctg ccccgccagc cgcaactcca 150
ccgtgagccg cctcatcttc acgtttcttc tcttcctggg ggtgctggtg 200
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250
ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300
tcgaactgtg ctccctgctt ggctaccggt ctgtctaccg catgtgcttc 350
gccacggcgg ccttcttctt cttctttttt accctgctca tgctctgcgt 400
gagcagcagc cgggaacccc gggctgccat ccagaatggg ttttggttct 450
ttaagttcct gatcctggtg ggcctcaccg tgggtgcctt ctacatccct 500
gacggtcctt tcacaaacat ctggttctac ttcggcgtcg tgggctcctt 550
cctcttcate ctcatccagc tgggtgctgt catcgacttt gcgcactcct 600
ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg 650
tacgcaggcc tcttcttctt cactctcttc ttctacttgc tgtcgatcgc 700
ggcgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750
agggcaaggt cttcatcagc ctcaacctca ccttctgtgt ctgcgtgtcc 800
atcgctgctg tcctgcccc ggtccaggac gccagccca actcgggtct 850
gctgcaggcc tcggtcatca ccctctacac catgtttgtc acctggtcag 900
ccctatccag tatccctgaa cagaaatgca acccccattt gccaaaccag 950

ctgggcaacg agacagttgt ggcaggcccc gagggctatg agaccagtg 1000
 gtgggatgcc ccgagcattg tgggcctcat catcttcctc ctgtgcaccc 1050
 tcttcatcag tctgcgctcc tcagaccacc ggcaggtgaa cagcctgatg 1100
 cagaccgagg agtgcaccacc tatgctagac gccacacagc agcagcagca 1150
 gcagggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200
 tcacctacag ctactccttc ttccaattct gcctgggtgct ggccctcactg 1250
 cacgtcatga tgacgctcac caactggtac aagcccgggtg agaccggaa 1300
 gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350
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 aaccgcgact tcagctgagg cagcctcaca gcctgccatc tggtgccctc 1450
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 ggggaactcc caccacagt gggcatccgg cactgaagcc ctggtgttcc 1800
 tggtcacgtc ccccagggga cctgcccc ttcttggtgact tcgtgcctta 1850
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900

a 1901

<210> 19

<211> 457

<212> PRT

<213> Homo sapiens

<400> 19

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				20					25					30

Ala	Ser	Arg	Asn	Ser	Thr	Val	Ser	Arg	Leu	Ile	Phe	Thr	Phe	Phe
				35					40					45

Leu	Phe	Leu	Gly	Val	Leu	Val	Ser	Ile	Ile	Met	Leu	Ser	Pro	Gly
				50					55					60

	350		355		360
Leu Asp Ala Thr	Gln Gln Gln Gln Gln	Gln Val Ala Ala Cys	Glu		
	365		370		375
Gly Arg Ala Phe	Asp Asn Glu Gln Asp	Gly Val Thr Tyr Ser	Tyr		
	380		385		390
Ser Phe Phe His	Phe Cys Leu Val Leu	Ala Ser Leu His Val	Met		
	395		400		405
Met Thr Leu Thr	Asn Trp Tyr Lys Pro	Gly Glu Thr Arg Lys	Met		
	410		415		420
Ile Ser Thr Trp	Thr Ala Val Trp Val	Lys Ile Cys Ala Ser	Trp		
	425		430		435
Ala Gly Leu Leu	Leu Tyr Leu Trp Thr	Leu Val Ala Pro Leu	Leu		
	440		445		450
Leu Arg Asn Arg	Asp Phe Ser				
	455				

<210> 20
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 20
 gccgcctcat cttcacgttc ttcc 24

<210> 21
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 21
 tcatccagct ggtgctgctc 20

<210> 22
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 22
 cttcttcac ttctgcctgg 20

<210> 23
 <211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 23
cctgggcaaa aatgcaac 18

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
caggaatgta gaaggcaccc acgg 24

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
tggcacagat cttcacccac acgg 24

<210> 26
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 27
gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50
ttaacctggg tcaaatgcac ggattctcac ctctacagt tacgtctctc 100
cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gtttgtccgt 150
aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250

Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val	35	40	45
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu	50	55	60
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala	65	70	75
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val	80	85	90
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile	95	100	105
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val	110	115	120
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly	125	130	135
Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	140	145	150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	155	160	165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	170	175	180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	185	190	195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	200	205	210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	215	220	225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	230	235	240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	245	250	255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	260	265	270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	275	280	285

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

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<400> 32
cttgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ataacgaatg aagcctcgtg 20

<210> 34
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 34
gctaatatct gtaagacggc agctacagca ggcatcattg 40

<210> 35
<211> 1819
<212> DNA
<213> Homo sapiens

<400> 35
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ccaccacagt ctgcgttgct gccccgcctg ggccaggccc caaaggcaag 100
gacaaagcag ctgtcaggga acctccgccg gagtccaatt tacgtgcagc 150
tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200
aagaactgcc tgtgcgccct caacctgctt tacaccttgg ttagtctgct 250
gctaattgga attgctgcgt ggggcattgg cttcgggctg atttccagtc 300
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gaatatgctg gagaggtttt gagatttggt ggtggcattg gcctgttctt 700

cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750
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 taagctccat ttgccagttt aaggaaggaa acactatctg gaaaagtacc 900
 ttattgatag tggaattata tatttttact ctatgtttct ctacatgttt 950
 ttttctttcc gttgctgaaa aatatttgaa acttgtggc tctgaagctc 1000
 ggtggcacct ggaatttact gtattcattg tcgggcactg tccactgtgg 1050
 cctttcttag cttttttacc tgcagaaaaa ctttgtatgg taccactgtg 1100
 ttggttatat ggtgaatctg aacgtacatc tcaactggtat aattatatgt 1150
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 taaaatcaga aagtatgaga tcctgttatg ttaagggaaa tccaaattcc 1250
 caattttttt tgggtctttt aggaaagatt gttgtggtaa aaagtgttag 1300
 tataaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350
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 acatttacct tcagcctcca tcagaatgga acgagttttg agtaatcagg 1500
 aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550
 aagactgcat ttttaaacia gttagtatta atgcgttggc ccacgtagca 1600
 aaaagatatt tgattatctt aaaaattgtt aaataccgtt ttcatgaaat 1650
 ttctcagtat tgtaacagca acttgtcaaa cctaagcata tttgaatatg 1700
 atctcccata atttgaaatt gaaatcgat tgtgtggctc tgtatattct 1750
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 taaaagaaag taatggaag 1819

<210> 36
 <211> 204
 <212> PRT
 <213> Homo sapiens

<400> 36
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 Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile
 20 25 30

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				35					40					45	
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala	
				50					55					60	
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu	
				65					70					75	
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe	
				80					85					90	
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly	
				95					100					105	
Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn	
				110					115					120	
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn	
				125					130					135	
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser	
				140					145					150	
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val	
				155					160					165	
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu	
				170					175					180	
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp	
				185					190					195	
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu							
				200											

<210> 37

<211> 390

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336

<223> unknown base

<400> 37

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tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150

aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200

gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250

gtgaccactn gtgctcgcca tgtgctcaa tcataggaga atatgctgga 300

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gatcctgggt gtttggctga cctacagata caggaaccag 390

<210> 38
<211> 566
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 27
<223> unknown base

<400> 38
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ggtaaaaagt gttagtataa aaatgataat ttacttgtag tcttttatga 100
ttacaccaat gtattctaga atagttatgt cttaggaaat tgtggtttta 150
tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200
tctaattgat aataacattt accttcagcc tcccatcaga atggaacgag 250
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400
ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450
gcatatttga atatgatctc ccataatttg aaattgaaat cgtatttgtgt 500
ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550
gttgtgcccc acttgc 566

<210> 39
<211> 264
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 84-85, 206
<223> unknown base

<400> 39
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cttgtttagc ccctgaaacc aggagcaaca gggnnacagct tccctggaggt 100
tggttggtgaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150
aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200

gacgctgcag tgtgagggac ctgtctgcac tgaggagagc agctgccaca 150
 cggaggatga cttgactgat gcaaggggaag ctggcttcca ggtcaaggcc 200
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<210> 45

<211> 359

<212> PRT

<213> Homo sapiens

<400> 45

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				20					25					30
Glu	Thr	Leu	Gln	Cys	Glu	Gly	Pro	Val	Cys	Thr	Glu	Glu	Ser	Ser
				35					40					45
Cys	His	Thr	Glu	Asp	Asp	Leu	Thr	Asp	Ala	Arg	Glu	Ala	Gly	Phe
				50					55					60
Gln	Val	Lys	Ala	Tyr	Thr	Phe	Ser	Glu	Pro	Phe	His	Leu	Ile	Val
				65					70					75
Ser	Tyr	Asp	Trp	Leu	Ile	Leu	Gln	Gly	Pro	Ala	Lys	Pro	Val	Phe
				80					85					90
Glu	Gly	Asp	Leu	Leu	Val	Leu	Arg	Cys	Gln	Ala	Trp	Gln	Asp	Trp
				95					100					105
Pro	Leu	Thr	Gln	Val	Thr	Phe	Tyr	Arg	Asp	Gly	Ser	Ala	Leu	Gly
				110					115					120
Pro	Pro	Gly	Pro	Asn	Arg	Glu	Phe	Ser	Ile	Thr	Val	Val	Gln	Lys
				125					130					135
Ala	Asp	Ser	Gly	His	Tyr	His	Cys	Ser	Gly	Ile	Phe	Gln	Ser	Pro
				140					145					150

Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	
				155					160					165	
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	
				170					175					180	
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	
				185					190					195	
Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	
				200					205					210	
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	
				215					220					225	
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	
				230					235					240	
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	
				245					250					255	
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	
				260					265					270	
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	
				275					280					285	
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	
				290					295					300	
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	
				305					310					315	
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	
				320					325					330	
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	
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Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		
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 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

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 <210> 47
 <211> 18
 <212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 47
tttccagcgc caattctc 18

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtcctcagtg gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
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<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

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ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100
gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150
gcacctaaaca gtggacactt atggccgtcc catcctggaa gtgccagaga 200
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ccoctgcaag gctacacca agtcttggtg aagtggctgg tacaacgtgg 300
ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc 350

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 cacgtgtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500
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<210> 52

<211> 321

<212> PRT

<213> Homo sapiens

<400> 52

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Asp	Thr	Tyr	Gly	Arg	Pro	Ile	Leu	Glu	Val	Pro	Glu	Ser	Val	Thr
				20					25					30
Gly	Pro	Trp	Lys	Gly	Asp	Val	Asn	Leu	Pro	Cys	Thr	Tyr	Asp	Pro
				35					40					45
Leu	Gln	Gly	Tyr	Thr	Gln	Val	Leu	Val	Lys	Trp	Leu	Val	Gln	Arg
				50					55					60
Gly	Ser	Asp	Pro	Val	Thr	Ile	Phe	Leu	Arg	Asp	Ser	Ser	Gly	Asp
				65					70					75
His	Ile	Gln	Gln	Ala	Lys	Tyr	Gln	Gly	Arg	Leu	His	Val	Ser	His
				80					85					90
Lys	Val	Pro	Gly	Asp	Val	Ser	Leu	Gln	Leu	Ser	Thr	Leu	Glu	Met
				95					100					105
Asp	Asp	Arg	Ser	His	Tyr	Thr	Cys	Glu	Val	Thr	Trp	Gln	Thr	Pro
				110					115					120
Asp	Gly	Asn	Gln	Val	Val	Arg	Asp	Lys	Ile	Thr	Glu	Leu	Arg	Val
				125					130					135
Gln	Lys	Leu	Ser	Val	Ser	Lys	Pro	Thr	Val	Thr	Thr	Gly	Ser	Gly
				140					145					150
Tyr	Gly	Phe	Thr	Val	Pro	Gln	Gly	Met	Arg	Ile	Ser	Leu	Gln	Cys
				155					160					165
Gln	Ala	Arg	Gly	Ser	Pro	Pro	Ile	Ser	Tyr	Ile	Trp	Tyr	Lys	Gln
				170					175					180

Gln	Thr	Asn	Asn	Gln	Glu	Pro	Ile	Lys	Val	Ala	Thr	Leu	Ser	Thr	
				185					190					195	
Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe	
				200					205					210	
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile	
				215					220					225	
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys	
				230					235					240	
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	
				245					250					255	
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	
				260					265					270	
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	
				275					280					285	
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	
				290					295					300	
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	
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Val	Tyr	Glu	Ala	Ala	Arg										
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<210> 53
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 53
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<210> 54
 <211> 21
 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 54
 gtcggaagac atcccaacaa g 21

<210> 55
 <211> 24
 <212> DNA
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<220>

<223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

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<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

tgatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

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cgcccggcac atggctgcag ccacctcgcg cgcaccccga ggccggcgcg 100

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caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350

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<210> 59
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 59
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 Val Thr Leu Pro Cys His His Gln Leu Gly Leu Pro Glu Lys Asp
 35 40 45
 Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln
 50 55 60
 Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu
 65 70 75
 Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu
 80 85 90
 Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp
 95 100 105
 Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val
 110 115 120
 Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro
 125 130 135
 Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr
 140 145 150
 Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr
 155 160 165
 Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro
 170 175 180

Pro	Lys	Ser	Arg	Ile	Asp	Tyr	Asn	His	Pro	Gly	Arg	Val	Leu	Leu	185	190	195
Gln	Asn	Leu	Thr	Met	Ser	Tyr	Ser	Gly	Leu	Tyr	Gln	Cys	Thr	Ala	200	205	210
Gly	Asn	Glu	Ala	Gly	Lys	Glu	Ser	Cys	Val	Val	Arg	Val	Thr	Val	215	220	225
Gln	Tyr	Val	Gln	Ser	Ile	Gly	Met	Val	Ala	Gly	Ala	Val	Thr	Gly	230	235	240
Ile	Val	Ala	Gly	Ala	Leu	Leu	Ile	Phe	Leu	Leu	Val	Trp	Leu	Leu	245	250	255
Ile	Arg	Arg	Lys	Asp	Lys	Glu	Arg	Tyr	Glu	Glu	Glu	Glu	Arg	Pro	260	265	270
Asn	Glu	Ile	Arg	Glu	Asp	Ala	Glu	Ala	Pro	Lys	Ala	Arg	Leu	Val	275	280	285
Lys	Pro	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Arg	Ser	Ser	Arg	Ser	Gly	290	295	300
Ser	Ser	Ser	Thr	Arg	Ser	Thr	Ala	Asn	Ser	Ala	Ser	Arg	Ser	Gln	305	310	315
Arg	Thr	Leu	Ser	Thr	Asp	Ala	Ala	Pro	Gln	Pro	Gly	Leu	Ala	Thr	320	325	330
Gln	Ala	Tyr	Ser	Leu	Val	Gly	Pro	Glu	Val	Arg	Gly	Ser	Glu	Pro	335	340	345
Lys	Lys	Val	His	His	Ala	Asn	Leu	Thr	Lys	Ala	Glu	Thr	Thr	Pro	350	355	360
Ser	Met	Ile	Pro	Ser	Gln	Ser	Arg	Ala	Phe	Gln	Thr	Val			365	370	

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- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 60
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- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe

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<211> 43

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<223> Synthetic oligonucleotide probe

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<212> DNA

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 <213> Homo sapiens

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 Arg Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu
 20 25 30

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Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	
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Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	
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Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	
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Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	
				95					100					105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	
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Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	
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Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	
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Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	
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Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	
				170					175					180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	
				185					190					195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	
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Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	
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Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	
				230					235					240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	
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Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	
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Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	
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Glu	Asp	Val	Asn	Lys	Thr	Leu	Pro	Asn	Leu	Gln	Val	Val	Asn	His	
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Gln	Gln	Gly	Pro	His	His	Arg	His	Ile	Leu	Lys	Leu	Leu	Pro	Ser	
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Pro	Lys	Arg	Gly	His 335	Pro	Arg	Gln	Asn	Leu	His	Lys	His	Phe	Asp 345
Ile	Asn	Glu	His	Leu 350	Pro	Trp	Met	Ile	Val 355	Leu	Phe	Leu	Leu	Leu 360
Val	Leu	Val	Val	Ile 365	Val	Val	Cys	Ser	Ile 370	Arg	Lys	Ser	Ser	Arg 375
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Leu	Val	Ala	Ala	Gln 425	Val	Gly	Ser	Gln	Trp 430	Lys	Asp	Ile	Tyr	Gln 435
Phe	Leu	Cys	Asn	Ala 440	Ser	Glu	Arg	Glu	Val 445	Ala	Ala	Phe	Ser	Asn 450
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Trp	Thr	Ile	Arg	Gly 470	Pro	Glu	Ala	Ser	Leu 475	Ala	Gln	Leu	Ile	Ser 480
Ala	Leu	Arg	Gln	His 485	Arg	Arg	Asn	Asp	Val 490	Val	Glu	Lys	Ile	Arg 495
Gly	Leu	Met	Glu	Asp 500	Thr	Thr	Gln	Leu	Glu 505	Thr	Asp	Lys	Leu	Ala 510
Leu	Pro	Met	Ser	Pro 515	Ser	Pro	Leu	Ser	Pro 520	Ser	Pro	Ile	Pro	Ser 525
Pro	Asn	Ala	Lys	Leu 530	Glu	Asn	Ser	Ala	Leu 535	Leu	Thr	Val	Glu	Pro 540
Ser	Pro	Gln	Asp	Lys 545	Asn	Lys	Gly	Phe	Phe 550	Val	Asp	Glu	Ser	Glu 555
Pro	Leu	Leu	Arg	Cys 560	Asp	Ser	Thr	Ser	Ser 565	Gly	Ser	Ser	Ala	Leu 570
Ser	Arg	Asn	Gly	Ser 575	Phe	Ile	Thr	Lys	Glu 580	Lys	Lys	Asp	Thr	Val 585
Leu	Arg	Gln	Val	Arg 590	Leu	Asp	Pro	Cys	Asp 595	Leu	Gln	Pro	Ile	Phe 600
Asp	Asp	Met	Leu	His 605	Phe	Leu	Asn	Pro	Glu 610	Glu	Leu	Arg	Val	Ile 615

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<211> 453

<212> PRT

<213> Homo sapiens

<400> 69

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				20					25					30
Pro	Asp	Ala	Asp	Ala	Val	Ala	Ala	Gln	Ile	Leu	Ser	Leu	Leu	Pro
				35					40					45
Leu	Lys	Phe	Phe	Pro	Ile	Ile	Val	Ile	Gly	Ile	Ile	Ala	Leu	Ile
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Leu	Ala	Leu	Ala	Ile	Gly	Leu	Gly	Ile	His	Phe	Asp	Cys	Ser	Gly
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Lys	Tyr	Arg	Cys	Arg	Ser	Ser	Phe	Lys	Cys	Ile	Glu	Leu	Ile	Ala
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Arg	Cys	Asp	Gly	Val	Ser	Asp	Cys	Lys	Asp	Gly	Glu	Asp	Glu	Tyr
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Arg	Cys	Val	Arg	Val	Gly	Gly	Gln	Asn	Ala	Val	Leu	Gln	Val	Phe

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Thr	Ala	Ala	Ser	Trp 125	Lys	Thr	Met	Cys	Ser 130	Asp	Asp	Trp	Lys	Gly 135
His	Tyr	Ala	Asn	Val 140	Ala	Cys	Ala	Gln	Leu 145	Gly	Phe	Pro	Ser	Tyr 150
Val	Ser	Ser	Asp	Asn 155	Leu	Arg	Val	Ser	Ser 160	Leu	Glu	Gly	Gln	Phe 165
Arg	Glu	Glu	Phe	Val 170	Ser	Ile	Asp	His	Leu 175	Leu	Pro	Asp	Asp	Lys 180
Val	Thr	Ala	Leu	His 185	His	Ser	Val	Tyr	Val 190	Arg	Glu	Gly	Cys	Ala 195
Ser	Gly	His	Val	Val 200	Thr	Leu	Gln	Cys	Thr 205	Ala	Cys	Gly	His	Arg 210
Arg	Gly	Tyr	Ser	Ser 215	Arg	Ile	Val	Gly	Gly 220	Asn	Met	Ser	Leu	Leu 225
Ser	Gln	Trp	Pro	Trp 230	Gln	Ala	Ser	Leu	Gln 235	Phe	Gln	Gly	Tyr	His 240
Leu	Cys	Gly	Gly	Ser 245	Val	Ile	Thr	Pro	Leu 250	Trp	Ile	Ile	Thr	Ala 255
Ala	His	Cys	Val	Tyr 260	Asp	Leu	Tyr	Leu	Pro 265	Lys	Ser	Trp	Thr	Ile 270
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Leu	Val	Glu	Lys	Ile 290	Val	Tyr	His	Ser	Lys 295	Tyr	Lys	Pro	Lys	Arg 300
Leu	Gly	Asn	Asp	Ile 305	Ala	Leu	Met	Lys	Leu 310	Ala	Gly	Pro	Leu	Thr 315
Phe	Asn	Glu	Met	Ile 320	Gln	Pro	Val	Cys	Leu 325	Pro	Asn	Ser	Glu	Glu 330
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Thr	Glu	Asp	Gly	Gly 350	Asp	Ala	Ser	Pro	Val 355	Leu	Asn	His	Ala	Ala 360
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Gly	Gly	Val	Asp	Ser 395	Cys	Gln	Gly	Asp	Ser 400	Gly	Gly	Pro	Leu	Val 405

Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe
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Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg
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<212> DNA
<213> Homo sapiens

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Arg Gln Gly Lys	Asp Leu Glu Lys Val	Lys Gln Arg Leu Ile	Glu
230		235	240
Ile Ala Asn His	Val Asp Lys Phe Tyr	Arg Pro Leu Asn Ile	Arg
245		250	255
Ile Val Leu Val	Gly Val Glu Val Trp	Asn Asp Met Asp Lys	Cys
260		265	270
Ser Val Ser Gln	Asp Pro Phe Thr Ser	Leu His Glu Phe Leu	Asp
275		280	285
Trp Arg Lys Met	Lys Leu Leu Pro Arg	Lys Ser His Asp Asn	Ala
290		295	300
Gln Leu Val Ser	Gly Val Tyr Phe Gln	Gly Thr Thr Ile Gly	Met
305		310	315
Ala Pro Ile Met	Ser Met Cys Thr Ala	Asp Gln Ser Gly Gly	Ile
320		325	330
Val Met Asp His	Ser Asp Asn Pro Leu	Gly Ala Ala Val Thr	Leu
335		340	345
Ala His Glu Leu	Gly His Asn Phe Gly	Met Asn His Asp Thr	Leu
350		355	360
Asp Arg Gly Cys	Ser Cys Gln Met Ala	Val Glu Lys Gly Gly	Cys
365		370	375
Ile Met Asn Ala	Ser Thr Gly Tyr Pro	Phe Pro Met Val Phe	Ser
380		385	390
Ser Cys Ser Arg	Lys Asp Leu Glu Thr	Ser Leu Glu Lys Gly	Met
395		400	405
Gly Val Cys Leu	Phe Asn Leu Pro Glu	Val Arg Glu Ser Phe	Gly
410		415	420
Gly Gln Lys Cys	Gly Asn Arg Phe Val	Glu Glu Gly Glu Glu	Cys
425		430	435
Asp Cys Gly Glu	Pro Glu Glu Cys Met	Asn Arg Cys Cys Asn	Ala
440		445	450
Thr Thr Cys Thr	Leu Lys Pro Asp Ala	Val Cys Ala His Gly	Leu
455		460	465
Cys Cys Glu Asp	Cys Gln Leu Lys Pro	Ala Gly Thr Ala Cys	Arg
470		475	480
Asp Ser Ser Asn	Ser Cys Asp Leu Pro	Glu Phe Cys Thr Gly	Ala
485		490	495
Ser Pro His Cys	Pro Ala Asn Val Tyr	Leu His Asp Gly His	Ser

				500					505					510			
Cys	Gln	Asp	Val	Asp 515	Gly	Tyr	Cys	Tyr	Asn 520	Gly	Ile	Cys	Gln	Thr 525			
His	Glu	Gln	Gln	Cys 530	Val	Thr	Leu	Trp	Gly 535	Pro	Gly	Ala	Lys	Pro 540			
Ala	Pro	Gly	Ile	Cys 545	Phe	Glu	Arg	Val	Asn 550	Ser	Ala	Gly	Asp	Pro 555			
Tyr	Gly	Asn	Cys	Gly 560	Lys	Val	Ser	Lys	Ser 565	Ser	Phe	Ala	Lys	Cys 570			
Glu	Met	Arg	Asp	Ala 575	Lys	Cys	Gly	Lys	Ile 580	Gln	Cys	Gln	Gly	Gly 585			
Ala	Ser	Arg	Pro	Val 590	Ile	Gly	Thr	Asn	Ala 595	Val	Ser	Ile	Glu	Thr 600			
Asn	Ile	Pro	Leu	Gln 605	Gln	Gly	Gly	Arg	Ile 610	Leu	Cys	Arg	Gly	Thr 615			
His	Val	Tyr	Leu	Gly 620	Asp	Asp	Met	Pro	Asp 625	Pro	Gly	Leu	Val	Leu 630			
Ala	Gly	Thr	Lys	Cys 635	Ala	Asp	Gly	Lys	Ile 640	Cys	Leu	Asn	Arg	Gln 645			
Cys	Gln	Asn	Ile	Ser 650	Val	Phe	Gly	Val	His 655	Glu	Cys	Ala	Met	Gln 660			
Cys	His	Gly	Arg	Gly 665	Val	Cys	Asn	Asn	Arg 670	Lys	Asn	Cys	His	Cys 675			
Glu	Ala	His	Trp	Ala 680	Pro	Pro	Phe	Cys	Asp 685	Lys	Phe	Gly	Phe	Gly 690			
Gly	Ser	Thr	Asp	Ser 695	Gly	Pro	Ile	Arg	Gln 700	Ala	Glu	Ala	Arg	Gln 705			
Glu	Ala	Ala	Glu	Ser 710	Asn	Arg	Glu	Arg	Gly 715	Gln	Gly	Gln	Glu	Pro 720			
Val	Gly	Ser	Gln	Glu 725	His	Ala	Ser	Thr	Ala 730	Ser	Leu	Thr	Leu	Ile 735			

58

tcccaaggct tcttgatgg cagatgattn tggggttttg cattgtttcc 50
 ctgacaacga aaacaaaaca gttttggggg ttcaggaggg gaantccagc 100
 ctaccagga agtttgcaga aacagtgcaa ggaagggcag ganttcctgg 150
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 agcaagggtt gggcccagtg tcccctttcc ccagtgcacac ctcagccttg 350
 gcagccctga taactggtn ntggctgcaa nttaatgctn tgatatggct 400
 ttttagcattt attatatgaa aatagcaggg ttttagtttt taatttatca 450
 gagaccctgc caccattcc atntccatcc aag 483

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 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 76
 gtctcagcac gtgttctggt ctcagg 27

<210> 77
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 77
 catgagcatg tgcacggc 18

<210> 78
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 78
 tacctgcacg atgggcac 18

<210> 79
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe
 <400> 79
 cactgggcac ctcccttc 18
 <210> 80
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe
 <400> 80
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 <210> 81
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe
 <400> 81
 tccctgttg actctgcagc ttcc 24
 <210> 82
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe
 <400> 82
 cttcgctggg aagagtttg 19
 <210> 83
 <211> 50
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<220>
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 <400> 83
 gtgcaaccaa cagatacaaa ctcttcccag cgaagaagct gaaaagcgtc 50
 <210> 84
 <211> 1714
 <212> DNA
 <213> Homo sapiens

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 gctactgcac tctagcctag cctgggcaac agagtgaac ttctgtctca 1400
 aaaaaaaaaa gccaaagtga gtggctcacg cctgtaatcc cggcactttg 1450
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<220>
<223> Synthetic oligonucleotide probe

<400> 88
gctccctacc cgtgcaggtt tcttcatttg ttcctttaac cagtatgccg 50

<210> 89
<211> 2956
<212> DNA
<213> Homo sapiens

<400> 89
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cgccctctcc cgctgctggc ccggccggcg gccctgactg cgctgctgct 100
gctgctgctg ggccatggcg gcggcgggcg ctggggcgcc cgggcccagg 150
aggcggcggc ggccggcgcg gacgggcccc ccgcggcaga cggcgaggac 200
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aacagcatgg aagatgccaa agtctatgtg gctaaagtgg actgcacggc 400
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tcaagattgg caaggttgat tgtacacagc actatgaact ctgctccgga 800
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 ttttaa 2956

<210> 90
 <211> 432
 <212> PRT
 <213> Homo sapiens

<400> 90
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 20 25 30
 Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala
 35 40 45
 Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro
 50 55 60
 His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile
 65 70 75
 Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly
 80 85 90
 His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys
 95 100 105
 Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp
 110 115 120
 Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly
 125 130 135
 Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys
 140 145 150
 Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu
 155 160 165
 Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu
 170 175 180

Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser	185	190	195
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile	200	205	210
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	215	220	225
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	230	235	240
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser	245	250	255
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	260	265	270
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	275	280	285
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly	290	295	300
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	305	310	315
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn	320	325	330
Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	335	340	345
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	350	355	360
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	365	370	375
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	380	385	390
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	395	400	405
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	410	415	420
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				425	430	

<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

	80	85	90
Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu	95	100	105
Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp	110	115	120
Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile	125	130	135
Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala	140	145	150
Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu	155	160	165
Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly	170	175	180
Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile	185	190	195
Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly	200	205	210
Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn	215	220	225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser	230	235	240
Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly	245	250	255
Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys	260	265	270
Glu Phe Ile Lys Lys Lys Lys	275		

<210> 98
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 98
 cgctgactat gttgcccaaga gtgg 24

<210> 99
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 99

gatgatggag gctccataacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

gtgttcattg gcgatgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

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ctcgacctcg acccacgcgt ccgctgctct ccgcccggtg ggagtgggtg 100

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gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200

agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250

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ctgctgctga agctacacct ctggccgcag ttgcgctggc ttccggcgga 350

cttggccttt gcggtgcgag ctctgtgctg caaaagggtt cttcgagctc 400

gcgccctggc cgcggctgcc gccgaccggg aagggtccga ggggggctgc 450

agcctggcct ggcgccctgc ggaactggcc cagcagcgcg ccgcgcacac 500

ctttctcatt cacggctcgc ggcgcttttag ctactcagag gcggagcgcg 550

agagtaacag ggctgcacgc gccttcctac gtgcgctagg ctgggactgg 600

ggaccogacg gcggcgacag cggcgagggg agcgctggag aaggcgagcg 650

ggcagcgccg ggagccggag atgcagcggc cggaagcggc gcggagtgtg 700

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 catggcccaa cttgtttatt gcag 2574

<210> 102
 <211> 730
 <212> PRT
 <213> Homo sapiens

<400> 102
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 Gln Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Gly Ser Gly
 20 25 30
 Met Phe Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala
 35 40 45
 Gly Ser Met Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu
 50 55 60
 Pro Leu Leu Leu Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp
 65 70 75
 Leu Pro Ala Asp Leu Ala Phe Ala Val Arg Ala Leu Cys Cys Lys
 80 85 90
 Arg Ala Leu Arg Ala Arg Ala Leu Ala Ala Ala Ala Asp Pro
 95 100 105
 Glu Gly Pro Glu Gly Gly Cys Ser Leu Ala Trp Arg Leu Ala Glu
 110 115 120
 Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser
 125 130 135
 Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala
 140 145 150
 Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp
 155 160 165
 Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala
 170 175 180
 Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe
 185 190 195
 Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala Ala Pro
 200 205 210

Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro	215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg	230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His	245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu	260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met	275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly	290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro	305	310	315
Val	Pro	Gly	Tyr	Leu	Ser	Ser	Pro	Gln	Ser	Ile	Thr	Asp	Thr	Cys	320	325	330
Leu	Tyr	Ile	Phe	Thr	Ser	Gly	Thr	Thr	Gly	Leu	Pro	Lys	Ala	Ala	335	340	345
Arg	Ile	Ser	His	Leu	Lys	Ile	Leu	Gln	Cys	Gln	Gly	Phe	Tyr	Gln	350	355	360
Leu	Cys	Gly	Val	His	Gln	Glu	Asp	Val	Ile	Tyr	Leu	Ala	Leu	Pro	365	370	375
Leu	Tyr	His	Met	Ser	Gly	Ser	Leu	Leu	Gly	Ile	Val	Gly	Cys	Met	380	385	390
Gly	Ile	Gly	Ala	Thr	Val	Val	Leu	Lys	Ser	Lys	Phe	Ser	Ala	Gly	395	400	405
Gln	Phe	Trp	Glu	Asp	Cys	Gln	Gln	His	Arg	Val	Thr	Val	Phe	Gln	410	415	420
Tyr	Ile	Gly	Glu	Leu	Cys	Arg	Tyr	Leu	Val	Asn	Gln	Pro	Pro	Ser	425	430	435
Lys	Ala	Glu	Arg	Gly	His	Lys	Val	Arg	Leu	Ala	Val	Gly	Ser	Gly	440	445	450
Leu	Arg	Pro	Asp	Thr	Trp	Glu	Arg	Phe	Val	Arg	Arg	Phe	Gly	Pro	455	460	465
Leu	Gln	Val	Leu	Glu	Thr	Tyr	Gly	Leu	Thr	Glu	Gly	Asn	Val	Ala	470	475	480
Thr	Ile	Asn	Tyr	Thr	Gly	Gln	Arg	Gly	Ala	Val	Gly	Arg	Ala	Ser	485	490	495
Trp	Leu	Tyr	Lys	His	Ile	Phe	Pro	Phe	Ser	Leu	Ile	Arg	Tyr	Asp			

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Val Thr Thr Gly Glu Pro Ile Arg Asp	Pro Gln Gly His Cys Met	
515	520	525
Ala Thr Ser Pro Gly Glu Pro Gly Leu	Leu Val Ala Pro Val Ser	
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Gln Gln Ser Pro Phe Leu Gly Tyr Ala	Gly Gly Pro Glu Leu Ala	
545	550	555
Gln Gly Lys Leu Leu Lys Asp Val Phe	Arg Pro Gly Asp Val Phe	
560	565	570
Phe Asn Thr Gly Asp Leu Leu Val Cys	Asp Asp Gln Gly Phe Leu	
575	580	585
Arg Phe His Asp Arg Thr Gly Asp Thr	Phe Arg Trp Lys Gly Glu	
590	595	600
Asn Val Ala Thr Thr Glu Val Ala Glu	Val Phe Glu Ala Leu Asp	
605	610	615
Phe Leu Gln Glu Val Asn Val Tyr Gly	Val Thr Val Pro Gly His	
620	625	630
Glu Gly Arg Ala Gly Met Ala Ala Leu	Val Leu Arg Pro Pro His	
635	640	645
Ala Leu Asp Leu Met Gln Leu Tyr Thr	His Val Ser Glu Asn Leu	
650	655	660
Pro Pro Tyr Ala Arg Pro Arg Phe Leu	Arg Leu Gln Glu Ser Leu	
665	670	675
Ala Thr Thr Glu Thr Phe Lys Gln Gln	Lys Val Arg Met Ala Asn	
680	685	690
Glu Gly Phe Asp Pro Ser Thr Leu Ser	Asp Pro Leu Tyr Val Leu	
695	700	705
Asp Gln Ala Val Gly Ala Tyr Leu Pro	Leu Thr Thr Ala Arg Tyr	
710	715	720
Ser Ala Leu Leu Ala Gly Asn Leu Arg	Ile	
725	730	

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<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

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 <211> 18
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 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 104
 ggagaatgtg gccacaac 18

 <210> 105
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 105
 gccctggcac agtgactcca tagacg 26

 <210> 106
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 106
 atccacttca gcggacac 18

 <210> 107
 <211> 45
 <212> DNA
 <213> Artificial Sequence

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 <223> Synthetic oligonucleotide probe

 <400> 107
 ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

 <210> 108
 <211> 2579
 <212> DNA
 <213> Homo sapiens

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 cctccacgca cacacatccc caagaacctc gagctcacac caacagacac 100

 acgcgcgcat acacactcgc tctcgtttgt ccatctccct cccgggggag 150

 ccggcgcgcg ctcccacctt tgccgcacac tccggcgagc cgagcccgca 200

gogctccagg attctgcggc tcggaactcg gattgcagct ctgaaccccc 250
 atggtgggtt tttaaact tcttttcctt ctcttcctcg ttttgattgc 300
 accgtttcca tctgggggct agaggagcaa ggcagcagcc ttcccagcca 350
 gcccttggtg gcttgccatc gtccatctgg cttataaaaag tttgctgagc 400
 gcagtccaga gggctgcgct gctcgtcccc tcggctggca gaagggggtg 450
 acgctgggca gcggcgagga gcgcgccgct gcctctggcg ggctttoggc 500
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 gatgaaactg catttttagct atctgaatgg ccaactcact tcttttctta 2300
 cactcttgga caatggacca tgccacaaaa acttaccggt tcttatgaga 2350
 agagagcagt aatgcaatct gcctcccttt ttgttttccc aaagagtacc 2400
 ggggtgccaga ctgaactgct tctcttttcc ttcagctatc tgtggggacc 2450
 ttgtttattc tagagagaat tcttactcaa atttttcgta ccaggagatt 2500
 ttcttacctt catttgcttt tatgctgcag aagtaaagga atctcacgtt 2550
 gtgaggggtt tttttttctc atttaaaat 2579

<210> 109
 <211> 555
 <212> PRT
 <213> Homo sapiens

<400> 109
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 Leu Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys
 20 25 30
 Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala
 35 40 45
 Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys
 50 55 60
 Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu
 65 70 75

Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150
Thr	Gly	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp	155	160	165
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Gln	Leu	Ile	Asn	Pro	Gln	Tyr	170	175	180
His	Phe	Ser	Glu	Asp	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Asp	185	190	195
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Ile	Gln	200	205	210
Val	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Arg	Thr	Phe	Val	Gln	Gly	Leu	215	220	225
Thr	Val	Gly	Arg	Glu	Val	Ala	Asn	Arg	Val	Ser	Lys	Val	Ser	Pro	230	235	240
Thr	Pro	Gly	Cys	Ile	Arg	Ala	Leu	Met	Lys	Met	Leu	Tyr	Cys	Pro	245	250	255
Tyr	Cys	Arg	Gly	Leu	Pro	Thr	Val	Arg	Pro	Cys	Asn	Asn	Tyr	Cys	260	265	270
Leu	Asn	Val	Met	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp	275	280	285
Thr	Glu	Trp	Asn	Leu	Phe	Ile	Asp	Ala	Met	Leu	Leu	Val	Ala	Glu	290	295	300
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile	305	310	315
Asp	Val	Lys	Ile	Ser	Glu	Ala	Ile	Met	Asn	Met	Gln	Glu	Asn	Ser	320	325	330
Met	Gln	Val	Ser	Ala	Lys	Val	Phe	Gln	Gly	Cys	Gly	Gln	Pro	Lys	335	340	345
Pro	Ala	Pro	Ala	Leu	Arg	Ser	Ala	Arg	Ser	Ala	Pro	Glu	Asn	Phe	350	355	360
Asn	Thr	Arg	Phe	Arg	Pro	Tyr	Asn	Pro	Glu	Glu	Arg	Pro	Thr	Thr			

365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu	Val Thr Asp Ile Lys Glu	
380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp	Ser Ala Leu Pro Tyr Thr	
395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala	Gly Thr Ser Asn Glu Glu	
410	415	420
Glu Cys Trp Asn Glu His Ser Lys Ala	Arg Tyr Leu Pro Glu Ile	
425	430	435
Met Asn Asp Gly Leu Thr Asn Gln Ile	Asn Asn Pro Glu Val Asp	
440	445	450
Val Asp Ile Thr Arg Pro Asp Thr Phe	Ile Arg Gln Gln Ile Met	
455	460	465
Ala Leu Arg Val Met Thr Asn Lys Leu	Lys Asn Ala Tyr Asn Gly	
470	475	480
Asn Asp Val Asn Phe Gln Asp Thr Ser	Asp Glu Ser Ser Gly Ser	
485	490	495
Gly Ser Gly Ser Gly Cys Met Asp Asp	Val Cys Pro Thr Glu Phe	
500	505	510
Glu Phe Val Thr Thr Glu Ala Pro Ala	Val Asp Pro Asp Arg Arg	
515	520	525
Glu Val Asp Ser Ser Ala Ala Gln Arg	Gly His Ser Leu Leu Ser	
530	535	540
Trp Ser Leu Thr Cys Ile Val Leu Ala	Leu Gln Arg Leu Cys Arg	
545	550	555

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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 110
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 <210> 111
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 111

tgacacagtct ctgcagtgcc cagg 24

<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgctg 40

<210> 113

<211> 4649

<212> DNA

<213> Homo sapiens

<400> 113

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 aataagttag ctgagaaaac gcacgcagtt tgcagcgcct gcgccgggtg 100
 cgccaactac gcaaagacca agcgggctcc gcgcggaccg gccgcggggc 150
 tagggaccgc gctttggcct tcaggctccc tagcagcggg gaaaaggaat 200
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<210> 114

<211> 515

<212> PRT

<213> Homo sapiens

<400> 114

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				20					25					30
Ala	Gly	Phe	Trp	Ile	Leu	Cys	Leu	Leu	Thr	Tyr	Gly	Tyr	Leu	Ser
				35					40					45
Trp	Gly	Gln	Ala	Leu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	Leu	Leu	Ala
				50					55					60
Gln	Ala	Gly	Glu	Lys	Leu	Glu	Pro	Ser	Thr	Thr	Ser	Thr	Ser	Gln
				65					70					75
Pro	His	Leu	Ile	Phe	Ile	Leu	Ala	Asp	Asp	Gln	Gly	Phe	Arg	Asp
				80					85					90
Val	Gly	Tyr	His	Gly	Ser	Glu	Ile	Lys	Thr	Pro	Thr	Leu	Asp	Lys
				95					100					105
Leu	Ala	Ala	Glu	Gly	Val	Lys	Leu	Glu	Asn	Tyr	Tyr	Val	Gln	Pro

				110					115					120
Ile	Cys	Thr	Pro	Ser 125	Arg	Ser	Gln	Phe	Ile 130	Thr	Gly	Lys	Tyr	Gln 135
Ile	His	Thr	Gly	Leu 140	Gln	His	Ser	Ile	Ile 145	Arg	Pro	Thr	Gln	Pro 150
Asn	Cys	Leu	Pro	Leu 155	Asp	Asn	Ala	Thr	Leu 160	Pro	Gln	Lys	Leu	Lys 165
Glu	Val	Gly	Tyr	Ser 170	Thr	His	Met	Val	Gly 175	Lys	Trp	His	Leu	Gly 180
Phe	Asn	Arg	Lys	Glu 185	Cys	Met	Pro	Thr	Arg 190	Arg	Gly	Phe	Asp	Thr 195
Phe	Phe	Gly	Ser	Leu 200	Leu	Gly	Ser	Gly	Asp 205	Tyr	Tyr	Thr	His	Tyr 210
Lys	Cys	Asp	Ser	Pro 215	Gly	Met	Cys	Gly	Tyr 220	Asp	Leu	Tyr	Glu	Asn 225
Asp	Asn	Ala	Ala	Trp 230	Asp	Tyr	Asp	Asn	Gly 235	Ile	Tyr	Ser	Thr	Gln 240
Met	Tyr	Thr	Gln	Arg 245	Val	Gln	Gln	Ile	Leu 250	Ala	Ser	His	Asn	Pro 255
Thr	Lys	Pro	Ile	Phe 260	Leu	Tyr	Thr	Ala	Tyr 265	Gln	Ala	Val	His	Ser 270
Pro	Leu	Gln	Ala	Pro 275	Gly	Arg	Tyr	Phe	Glu 280	His	Tyr	Arg	Ser	Ile 285
Ile	Asn	Ile	Asn	Arg 290	Arg	Arg	Tyr	Ala	Ala 295	Met	Leu	Ser	Cys	Leu 300
Asp	Glu	Ala	Ile	Asn 305	Asn	Val	Thr	Leu	Ala 310	Leu	Lys	Thr	Tyr	Gly 315
Phe	Tyr	Asn	Asn	Ser 320	Ile	Ile	Ile	Tyr	Ser 325	Ser	Asp	Asn	Gly	Gly 330
Gln	Pro	Thr	Ala	Gly 335	Gly	Ser	Asn	Trp	Pro 340	Leu	Arg	Gly	Ser	Lys 345
Gly	Thr	Tyr	Trp	Glu 350	Gly	Gly	Ile	Arg	Ala 355	Val	Gly	Phe	Val	His 360
Ser	Pro	Leu	Leu	Lys 365	Asn	Lys	Gly	Thr	Val 370	Cys	Lys	Glu	Leu	Val 375
His	Ile	Thr	Asp	Trp 380	Tyr	Pro	Thr	Leu	Ile 385	Ser	Leu	Ala	Glu	Gly 390
Gln	Ile	Asp	Glu	Asp 395	Ile	Gln	Leu	Asp	Gly 400	Tyr	Asp	Ile	Trp	Glu 405

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<210> 118
<211> 2260
<212> DNA
<213> Homo sapiens

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<221> unsure
<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086
<223> unknown base

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gccttgcgct cccgctgctg ctctcctggg tggcaggtgg tttcggaac 200
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atctttccnc attatattat aaaatntgga aangtcagtt tatctcccct 2050
cctcngtata tctgatttgt atangtangt tgatgngctt ctctctacaa 2100
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ctcttatgat acttcttgga aactatgaca tcaaagatag acttttgcct 2200
aagtggctta gctgggtctt tcatagccaa acttgatat ttaattcttt 2250
gtaataataa 2260

<210> 119
<211> 338
<212> PRT
<213> Homo sapiens

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Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	
				35					40					45	
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	
				50					55					60	
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
				65					70					75	
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	
				80					85					90	
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
				95					100					105	
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	
				110					115					120	
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	
				125					130					135	
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	
				140					145					150	
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	
				155					160					165	
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	
				170					175					180	
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
				185					190					195	
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	
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Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	
				215					220					225	
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	
				230					235					240	
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	
				245					250					255	
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	
				260					265					270	
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	
				275					280					285	
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
				290					295					300	
Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	

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 caacaatggt ggaatgtccc agcgtttctt gtgcatggat accagcttgg 450
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<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

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			20					25						30
Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
			35					40						45
Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
			50					55						60
Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val
			65					70						75
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly

	80	85	90
Met Ser Gln Arg	Ser 95	Leu Cys Met Asp Thr 100	Ser Leu Asp Val Tyr 105
Arg Lys Leu Ile	Glu 110	Leu Asn Tyr Leu Gly 115	Thr Val Ser Leu Thr 120
Lys Cys Val Leu	Pro 125	His Met Ile Glu Arg 130	Lys Gln Gly Lys Ile 135
Val Thr Val Asn	Ser 140	Ile Leu Gly Ile Ile 145	Ser Val Pro Leu Ser 150
Ile Gly Tyr Cys	Ala 155	Ser Lys His Ala Leu Arg 160	Gly Phe Phe Asn 165
Gly Leu Arg Thr	Glu 170	Leu Ala Thr Tyr Pro Gly 175	Ile Ile Val Ser 180
Asn Ile Cys Pro	Gly 185	Pro Val Gln Ser Asn 190	Ile Val Glu Asn Ser 195
Leu Ala Gly Glu	Val 200	Thr Lys Thr Ile Gly 205	Asn Asn Gly Asp Gln 210
Ser His Lys Met	Thr 215	Thr Ser Arg Cys Val 220	Arg Leu Met Leu Ile 225
Ser Met Ala Asn	Asp 230	Leu Lys Glu Val Trp 235	Ile Ser Glu Gln Pro 240
Phe Leu Leu Val	Thr 245	Tyr Leu Trp Gln Tyr 250	Met Pro Thr Trp Ala 255
Trp Trp Ile Thr	Asn 260	Lys Met Gly Lys Lys 265	Arg Ile Glu Asn Phe 270
Lys Ser Gly Val	Asp 275	Ala Asp Ser Ser Tyr 280	Phe Lys Ile Phe Lys 285
Thr Lys His Asp			

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 125
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<210> 126
 <211> 19
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatggggc gagtggcagg gacgacgcc agaag 46

<210> 131

<211> 2365

<212> DNA

<213> Homo sapiens

<400> 131

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<210> 132
 <211> 571
 <212> PRT
 <213> Homo sapiens

<400> 132
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 20 25 30
 Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe
 35 40 45
 Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn
 50 55 60
 Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln
 65 70 75

Gly	Ala	His	Ile	Cys 80	Ser	Gly	Ser	Leu	Val 85	Ala	Asp	Thr	Trp	Val 90
Leu	Thr	Ala	Ala	His 95	Cys	Phe	Glu	Lys	Ala 100	Ala	Ala	Thr	Glu	Leu 105
Asn	Ser	Trp	Ser	Val 110	Val	Leu	Gly	Ser	Leu 115	Gln	Arg	Glu	Gly	Leu 120
Ser	Pro	Gly	Ala	Glu 125	Glu	Val	Gly	Val	Ala 130	Ala	Leu	Gln	Leu	Pro 135
Arg	Ala	Tyr	Asn	His 140	Tyr	Ser	Gln	Gly	Ser 145	Asp	Leu	Ala	Leu	Leu 150
Gln	Leu	Ala	His	Pro 155	Thr	Thr	His	Thr	Pro 160	Leu	Cys	Leu	Pro	Gln 165
Pro	Ala	His	Arg	Phe 170	Pro	Phe	Gly	Ala	Ser 175	Cys	Trp	Ala	Thr	Gly 180
Trp	Asp	Gln	Asp	Thr 185	Ser	Asp	Ala	Pro	Gly 190	Thr	Leu	Arg	Asn	Leu 195
Arg	Leu	Arg	Leu	Ile 200	Ser	Arg	Pro	Thr	Cys 205	Asn	Cys	Ile	Tyr	Asn 210
Gln	Leu	His	Gln	Arg 215	His	Leu	Ser	Asn	Pro 220	Ala	Arg	Pro	Gly	Met 225
Leu	Cys	Gly	Gly	Pro 230	Gln	Pro	Gly	Val	Gln 235	Gly	Pro	Cys	Gln	Gly 240
Asp	Ser	Gly	Gly	Pro 245	Val	Leu	Cys	Leu	Glu 250	Pro	Asp	Gly	His	Trp 255
Val	Gln	Ala	Gly	Ile 260	Ile	Ser	Phe	Ala	Ser 265	Ser	Cys	Ala	Gln	Glu 270
Asp	Ala	Pro	Val	Leu 275	Leu	Thr	Asn	Thr	Ala 280	Ala	His	Ser	Ser	Trp 285
Leu	Gln	Ala	Arg	Val 290	Gln	Gly	Ala	Ala	Phe 295	Leu	Ala	Gln	Ser	Pro 300
Glu	Thr	Pro	Glu	Met 305	Ser	Asp	Glu	Asp	Ser 310	Cys	Val	Ala	Cys	Gly 315
Ser	Leu	Arg	Thr	Ala 320	Gly	Pro	Gln	Ala	Gly 325	Ala	Pro	Ser	Pro	Trp 330
Pro	Trp	Glu	Ala	Arg 335	Leu	Met	His	Gln	Gly 340	Gln	Leu	Ala	Cys	Gly 345
Gly	Ala	Leu	Val	Ser 350	Glu	Glu	Ala	Val	Leu 355	Thr	Ala	Ala	His	Cys 360
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly

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Thr	Arg	Pro	Glu	Glu 380	Trp	Gly	Leu	Lys	Gln 385	Leu	Ile	Leu	His	Gly 390
Ala	Tyr	Thr	His	Pro 395	Glu	Gly	Gly	Tyr	Asp 400	Met	Ala	Leu	Leu	Leu 405
Leu	Ala	Gln	Pro	Val 410	Thr	Leu	Gly	Ala	Ser 415	Leu	Arg	Pro	Leu	Cys 420
Leu	Pro	Tyr	Pro	Asp 425	His	His	Leu	Pro	Asp 430	Gly	Glu	Arg	Gly	Trp 435
Val	Leu	Gly	Arg	Ala 440	Arg	Pro	Gly	Ala	Gly 445	Ile	Ser	Ser	Leu	Gln 450
Thr	Val	Pro	Val	Thr 455	Leu	Leu	Gly	Pro	Arg 460	Ala	Cys	Ser	Arg	Leu 465
His	Ala	Ala	Pro	Gly 470	Gly	Asp	Gly	Ser	Pro 475	Ile	Leu	Pro	Gly	Met 480
Val	Cys	Thr	Ser	Ala 485	Val	Gly	Glu	Leu	Pro 490	Ser	Cys	Glu	Gly	Leu 495
Ser	Gly	Ala	Pro	Leu 500	Val	His	Glu	Val	Arg 505	Gly	Thr	Trp	Phe	Leu 510
Ala	Gly	Leu	His	Ser 515	Phe	Gly	Asp	Ala	Cys 520	Gln	Gly	Pro	Ala	Arg 525
Pro	Ala	Val	Phe	Thr 530	Ala	Leu	Pro	Ala	Tyr 535	Glu	Asp	Trp	Val	Ser 540
Ser	Leu	Asp	Trp	Gln 545	Val	Tyr	Phe	Ala	Glu 550	Glu	Pro	Glu	Pro	Glu 555
Ala	Glu	Pro	Gly	Ser 560	Cys	Leu	Ala	Asn	Ile 565	Ser	Gln	Pro	Thr	Ser 570

Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

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 attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

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Val	Gln	Val	Pro	Glu 35	Asp	Pro	Val	Val	Ala 40	Leu	Val	Gly	Thr	Asp 45	
Ala	Thr	Leu	Cys	Cys 50	Ser	Phe	Ser	Pro	Glu 55	Pro	Gly	Phe	Ser	Leu 60	
Ala	Gln	Leu	Asn	Leu 65	Ile	Trp	Gln	Leu	Thr 70	Asp	Thr	Lys	Gln	Leu 75	
Val	His	Ser	Phe	Ala 80	Glu	Gly	Gln	Asp	Gln 85	Gly	Ser	Ala	Tyr	Ala 90	
Asn	Arg	Thr	Ala	Leu 95	Phe	Pro	Asp	Leu	Leu 100	Ala	Gln	Gly	Asn	Ala 105	
Ser	Leu	Arg	Leu	Gln 110	Arg	Val	Arg	Val	Ala 115	Asp	Glu	Gly	Ser	Phe 120	
Thr	Cys	Phe	Val	Ser 125	Ile	Arg	Asp	Phe	Gly 130	Ser	Ala	Ala	Val	Ser 135	
Leu	Gln	Val	Ala	Ala 140	Pro	Tyr	Ser	Lys	Pro 145	Ser	Met	Thr	Leu	Glu 150	
Pro	Asn	Lys	Asp	Leu 155	Arg	Pro	Gly	Asp	Thr 160	Val	Thr	Ile	Thr	Cys 165	
Ser	Ser	Tyr	Gln	Gly 170	Tyr	Pro	Glu	Ala	Glu 175	Val	Phe	Trp	Gln	Asp 180	
Gly	Gln	Gly	Val	Pro 185	Leu	Thr	Gly	Asn	Val 190	Thr	Thr	Ser	Gln	Met 195	
Ala	Asn	Glu	Gln	Gly 200	Leu	Phe	Asp	Val	His 205	Ser	Val	Leu	Arg	Val 210	
Val	Leu	Gly	Ala	Asn 215	Gly	Thr	Tyr	Ser	Cys 220	Leu	Val	Arg	Asn	Pro 225	
Val	Leu	Gln	Gln	Asp 230	Ala	His	Xaa	Ser	Val 235	Thr	Ile	Thr	Gly	Gln 240	
Pro	Met	Thr	Phe	Pro 245	Pro	Glu	Ala	Leu	Trp 250	Val	Thr	Val	Gly	Leu 255	
Ser	Val	Cys	Leu	Ile 260	Ala	Leu	Leu	Val	Ala 265	Leu	Ala	Phe	Val	Cys 270	
Trp	Arg	Lys	Ile	Lys 275	Gln	Ser	Cys	Glu	Glu 280	Glu	Asn	Ala	Gly	Ala 285	
Glu	Asp	Gln	Asp	Gly 290	Glu	Gly	Glu	Gly	Ser 295	Lys	Thr	Ala	Leu	Gln 300	

Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
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Ala

<210> 138
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 138
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<210> 139
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 <212> DNA
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<220>
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<400> 139
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<210> 140
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<220>
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<400> 140
 ggacacagta tactgaccac 20

<210> 141
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 <212> DNA
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<220>
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<400> 141
 tgccaaccag gcagctgtaa gtgc 24

<210> 142
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

099840650

<400> 142
tggaagaaga ggggtggtgat gtgg 24

<210> 143
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 143
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<210> 144
<211> 2336
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1620, 1673
<223> unknown base

<400> 144
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tacgttctta aatctatgaa gtcgagggac ctttcgctgc tttttagagg 150
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gtttaccctg ggcatcctgg aggctctcaa aggttgggac cagggcttga 450
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gagttataga gatacatcta cccttttaat atagcactca totttcaaga 850

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<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

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20 25 30

Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly
35 40 45

Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly
50 55 60

Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile
65 70 75

Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln
80 85 90

Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile
95 100 105

Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro
110 115 120

Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg
125 130 135

Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn
140 145 150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys
155 160 165

Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His
170 175 180

Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys
185 190 195

Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu
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Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

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<220>
<223> Synthetic oligonucleotide probe

<400> 146
ctttccttgc ttcagcaaca tgaggc 26

<210> 147
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 147
gcccagagca ggaggaatga tgagc 25

<210> 148
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 148
gtggaacgcg gtcttgactc tggtcgtcac ttctttgatt ggggctttg 49

<210> 149
<211> 2196
<212> DNA
<213> Homo sapiens

<400> 149
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<210> 150
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 150

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Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp	35	40	45	
Ala	Arg	Leu	Pro	Cys	Thr	Phe	Asn	Ser	Cys	Tyr	Thr	Val	Asn	His	50	55	60	
Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys	65	70	75	
Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu	80	85	90	
Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro	95	100	105	
Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu	110	115	120	
Asp	Glu	Gly	Ile	Tyr	Asn	Cys	Tyr	Ile	Met	Asn	Pro	Pro	Asp	Arg	125	130	135	
His	Arg	Gly	His	Gly	Lys	Ile	His	Leu	Gln	Val	Leu	Met	Glu	Glu	140	145	150	
Pro	Pro	Glu	Arg	Asp	Ser	Thr	Val	Ala	Val	Ile	Val	Gly	Ala	Ser	155	160	165	
Val	Gly	Gly	Phe	Leu	Ala	Val	Val	Ile	Leu	Val	Leu	Met	Val	Val	170	175	180	
Lys	Cys	Val	Arg	Arg	Lys	Lys	Glu	Gln	Lys	Leu	Ser	Thr	Asp	Asp	185	190	195	
Leu	Lys	Thr	Glu	Glu	Glu	Gly	Lys	Thr	Asp	Gly	Glu	Gly	Asn	Pro	200	205	210	
Asp	Asp	Gly	Ala	Lys	215													

<210> 151

<210> 153
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 153
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<210> 154
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 154
 gcacgtttct cagcatcacc gac 23

<210> 155
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 156
 <211> 2680
 <212> DNA
 <213> Homo sapiens

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Ser Tyr Phe His	Thr Met Val Glu Ser	Leu Val Gly Trp Gly	Tyr		
	140	145	150		
Thr Arg Gly Glu	Asp Val Arg Gly Ala	Pro Tyr Asp Trp Arg	Arg		
	155	160	165		
Ala Pro Asn Glu	Asn Gly Pro Tyr Phe	Leu Ala Leu Arg Glu	Met		
	170	175	180		
Ile Glu Glu Met	Tyr Gln Leu Tyr Gly	Gly Pro Val Val Leu	Val		
	185	190	195		
Ala His Ser Met	Gly Asn Met Tyr Thr	Leu Tyr Phe Leu Gln	Arg		
	200	205	210		
Gln Pro Gln Ala	Trp Lys Asp Lys Tyr	Ile Arg Ala Phe Val	Ser		
	215	220	225		
Leu Gly Ala Pro	Trp Gly Gly Val Ala	Lys Thr Leu Arg Val	Leu		
	230	235	240		
Ala Ser Gly Asp	Asn Asn Arg Ile Pro	Val Ile Gly Pro Leu	Lys		
	245	250	255		
Ile Arg Glu Gln	Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu	Leu		
	260	265	270		
Pro Tyr Asn Tyr	Thr Trp Ser Pro Glu	Lys Val Phe Val Gln	Thr		
	275	280	285		
Pro Thr Ile Asn	Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe	Gln		
	290	295	300		
Asp Ile Gly Phe	Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr	Glu		
	305	310	315		
Gly Leu Val Glu	Ala Thr Met Pro Pro	Gly Val Gln Leu His	Cys		
	320	325	330		
Leu Tyr Gly Thr	Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr	Glu		
	335	340	345		
Ser Phe Pro Asp	Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly	Asp		
	350	355	360		
Gly Thr Val Asn	Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp	Gln		
	365	370	375		
Ser Arg Gln Glu	His Gln Val Leu Leu	Gln Glu Leu Pro Gly	Ser		
	380	385	390		
Glu His Ile Glu	Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr	Leu		
	395	400	405		

Lys Arg Val Leu Leu Gly Pro
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<210> 158
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 158
ctggggctac acacggggtg agg 23

<210> 159
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 159
ggtgccgctg cagaaagtag agcg 24

<210> 160
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 160
gccccaaatg aaaacggggc ctacttcctg gccctccgag agatg 45

<210> 161
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 161
cgagcgcgtg ggcggacgag tggggcgagg gcagcggcgg cgacggcgac 50
atggagagcg gggcctacgg cgcggccaag gcgggaggct ccttcgacct 100
gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150
tcttcgcctt gatcgtgttc tctgcatct atggtgagg ctacagcaat 200
gccacgagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250
ctgccgctat ggcagtgcca tcgggggtgct ggccttcctg gcctcgacct 300
tcttcttggg ggtcgacgag tatttcccc agatcagcaa cgccactgac 350
cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400

cctgtggttt gttggtttct gcttctcac caaccagtgg gcagtcacca 450
 acccgaagga cgtgctggtg ggggccgact ctgtgagggc agccatcacc 500
 ttcagcttct tttccatctt ctctgggggt gtgctggcct ccctggccta 550
 ccagcgctac aaggctggcg tggacgactt catccagaat tacgttgacc 600
 ccactcogga ccccaacact gcctacgcct cctaccaggg tgcatctgtg 650
 gacaactacc aacagccacc cttcaccag aacgcggaga ccaccgaggg 700
 ctaccagccg cccctgtgt actgagtggc ggtagcgtg ggaaggggga 750
 cagagagggc cctccctct gccctggact ttcccatcag cctcctggaa 800
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 gtgccccatg gctcccagac tctgtctgtg ccgagtgtat tataaaatcg 1450
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 tctcattcaa ag 1512

<210> 162
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 162
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 Asp Leu Arg Arg Phe Leu Thr Gln Pro Gln Val Val Ala Arg Ala
 20 25 30

Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly	
				35					40					45	
Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val	
				50					55					60	
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly	
				65					70					75	
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala	
				80					85					90	
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val	
				95					100					105	
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe	
				110					115					120	
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro	
				125					130					135	
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr	
				140					145					150	
Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly	Val	Leu	Ala	Ser	Leu	
				155					160					165	
Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp	Phe	Ile	Gln	Asn	
				170					175					180	
Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr	Ala	Ser	Tyr	
				185					190					195	
Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe	Thr	Gln	
				200					205					210	
Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr		
				215					220						

<210> 163
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 163
 tgggtotctgc cttgatcgtg ttct 24

<210> 164
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<400> 164
gtgtactgag cggcggttag 20

<210> 165
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 165
ctgaaggtga tggctgccct cac 23

<210> 166
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 166
ccaggaggct catgggaaag tcc 23

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
ccacgagtct aagcagatgt actgcgtggt caaccgcaac gaggatgcct 50

<210> 168
<211> 3143
<212> DNA
<213> Homo sapiens

<400> 168
gagccaccta cctgtctccg aggccaggcc tgcagggcct catcggccag 50
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ctggcggggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150
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cctggtgccc ctgtttgtgc tgctggccct gctcgtgctg gcttcggcgg 250
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caggtgtact caggcagtct gcgtgtactc aatcgccact totcccagga 350
tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400

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agaagatgct caaggagctc atcaccagca cccgcctggg aacttactac 450
aactccagct ccgctctattc ctttggggag ggacccctca cctgcttctt 500
ctgggttcatt ctccaaatcc ccgagcaccg ccggctgatg ctgagccccg 550
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agtgatcctg gaagccagtg tgaaagacat agctgcattg aattccacgc 700
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 tttggaataa agctgcctga tcaaaaaaaaa aaaaaaaaaa aaa 3143

<210> 169
 <211> 802
 <212> PRT
 <213> Homo sapiens
 <400> 169

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp	
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Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala	
				20					25					30	
Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	
				35					40					45	
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	
				50					55					60	
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	
				65					70					75	
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	
				80					85					90	
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	
				95					100					105	
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	
				110					115					120	
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly	
				125					130					135	
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro	
				140					145					150	
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu	
				155					160					165	
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val	
				170					175					180	
Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile	
				185					190					195	
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu	
				200					205					210	
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg	
				215					220					225	
Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	
				230					235					240	
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	
				245					250					255	
Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly	
				260					265					270	
Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg	
				275					280					285	
Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala	

	290		295		300
Val Val Trp Lys	Lys Gly Leu His Ser	Tyr Tyr Asp Pro Phe	Val		
	305		310		315
Leu Ser Val Gln	Pro Val Val Phe Gln	Ala Cys Glu Val Asn	Leu		
	320		325		330
Thr Leu Asp Asn	Arg Leu Asp Ser Gln	Gly Val Leu Ser Thr	Pro		
	335		340		345
Tyr Phe Pro Ser	Tyr Tyr Ser Pro Gln	Thr His Cys Ser Trp	His		
	350		355		360
Leu Thr Val Pro	Ser Leu Asp Tyr Gly	Leu Ala Leu Trp Phe	Asp		
	365		370		375
Ala Tyr Ala Leu	Arg Arg Gln Lys Tyr	Asp Leu Pro Cys Thr	Gln		
	380		385		390
Gly Gln Trp Thr	Ile Gln Asn Arg Arg	Leu Cys Gly Leu Arg	Ile		
	395		400		405
Leu Gln Pro Tyr	Ala Glu Arg Ile Pro	Val Val Ala Thr Ala	Gly		
	410		415		420
Ile Thr Ile Asn	Phe Thr Ser Gln Ile	Ser Leu Thr Gly Pro	Gly		
	425		430		435
Val Arg Val His	Tyr Gly Leu Tyr Asn	Gln Ser Asp Pro Cys	Pro		
	440		445		450
Gly Glu Phe Leu	Cys Ser Val Asn Gly	Leu Cys Val Pro Ala	Cys		
	455		460		465
Asp Gly Val Lys	Asp Cys Pro Asn Gly	Leu Asp Glu Arg Asn	Cys		
	470		475		480
Val Cys Arg Ala	Thr Phe Gln Cys Lys	Glu Asp Ser Thr Cys	Ile		
	485		490		495
Ser Leu Pro Lys	Val Cys Asp Gly Gln	Pro Asp Cys Leu Asn	Gly		
	500		505		510
Ser Asp Glu Glu	Gln Cys Gln Glu Gly	Val Pro Cys Gly Thr	Phe		
	515		520		525
Thr Phe Gln Cys	Glu Asp Arg Ser Cys	Val Lys Lys Pro Asn	Pro		
	530		535		540
Gln Cys Asp Gly	Arg Pro Asp Cys Arg	Asp Gly Ser Asp Glu	Glu		
	545		550		555
His Cys Asp Cys	Gly Leu Gln Gly Pro	Ser Ser Arg Ile Val	Gly		
	560		565		570
Gly Ala Val Ser	Ser Glu Gly Glu Trp	Pro Trp Gln Ala Ser	Leu		
	575		580		585

Gln Val Arg Gly	Arg His Ile Cys Gly	Gly Ala Leu Ile Ala Asp	590	595	600
Arg Trp Val Ile	Thr Ala Ala His Cys	Phe Gln Glu Asp Ser Met	605	610	615
Ala Ser Thr Val	Leu Trp Thr Val Phe	Leu Gly Lys Val Trp Gln	620	625	630
Asn Ser Arg Trp	Pro Gly Glu Val Ser	Phe Lys Val Ser Arg Leu	635	640	645
Leu Leu His Pro	Tyr His Glu Glu Asp	Ser His Asp Tyr Asp Val	650	655	660
Ala Leu Leu Gln	Leu Asp His Pro Val	Val Arg Ser Ala Ala Val	665	670	675
Arg Pro Val Cys	Leu Pro Ala Arg Ser	His Phe Phe Glu Pro Gly	680	685	690
Leu His Cys Trp	Ile Thr Gly Trp Gly	Ala Leu Arg Glu Gly Gly	695	700	705
Pro Ile Ser Asn	Ala Leu Gln Lys Val	Asp Val Gln Leu Ile Pro	710	715	720
Gln Asp Leu Cys	Ser Glu Ala Tyr Arg	Tyr Gln Val Thr Pro Arg	725	730	735
Met Leu Cys Ala	Gly Tyr Arg Lys Gly	Lys Lys Asp Ala Cys Gln	740	745	750
Gly Asp Ser Gly	Gly Pro Leu Val Cys	Lys Ala Leu Ser Gly Arg	755	760	765
Trp Phe Leu Ala	Gly Leu Val Ser Trp	Gly Leu Gly Cys Gly Arg	770	775	780
Pro Asn Tyr Phe	Gly Val Tyr Thr Arg	Ile Thr Gly Val Ile Ser	785	790	795
Trp Ile Gln Gln	Val Val Thr		800		

<210> 170
 <211> 1327
 <212> DNA
 <213> Homo sapiens

<400> 170
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 caccatcaac ttcacctccc agatctccct caccgggccc ggtgtgcggg 150
 tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200

tgttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250
 ccccaacggc ctggatgaga gaaactgcgt ttgcagagcc acattccagt 300
 gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggcag 350
 cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400
 atgtgggaca ttacacttcc agtgtgagga ccggagctgc gtgaagaagc 450
 ccaaccgcga gtgtgatggg cggcccgact gcagggacgg ctccgatgag 500
 gagcactgtg actgtggcct ccagggcccc tccagccgca ttgttggtgg 550
 agctgtgtcc tccgaggggt agtggccatg gcaggccagc ctccagggtc 600
 ggggtcgaca catctgtggg ggggccctca tcgctgaccg ctgggtgata 650
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 cccgcatcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250
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<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccaactgcttc cagg 24

<210> 172

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 172
taatccagca gtgcaggccg gg 22

<210> 173
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 173
atggcctcca cgggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 174
tgcctatgca ctgaggaggc agaag 25

<210> 175
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 175
aggcagggac acagagtcca ttcac 25

<210> 176
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 176
agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177
<211> 1510
<212> DNA
<213> Homo sapiens

<400> 177

ggacgagggc agatctcggt ctggggcaag ccgttgacac tcgctccctg 50
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gctggaaaca ccaagagggt gtttttggtt tttaaaactt ctgtttcttg 200
ggaggggggtg tggcggggca ggatgagcaa ctccgttcct ctgctctgtt 250
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ccagagggac ggctggaaga taagctccac aaaccctaaag ctacacagac 350
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tgcatgtcct aggaaaagga atctttacaa aataaacagt gtggaccct 1450

Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
				245					250					255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
				275					280					285
Val	Asn	Gln	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	Ser
				290					295					300
Asn	Arg	Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg
				305					310					315
Cys	Asn	Ser	Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg
				320					325					330
Asn	Ser	Lys	Met	Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg
				335					340					345
Gly	Asn	Leu	Gln	Ser	Leu	Glu	Cys	Pro						
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<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gtgagcatga gcgagccgctc cac 23

<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

gctattacaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240
 <212> DNA
 <213> Homo sapiens

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 acgcgctgga ggagtggagc agcaccgggc cggccctggg ggctgacagt 150
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 tcagtaagtt gagggtcaaaa ataaaggaat catacatctc 3240

<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met	Leu	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Ala	Leu
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Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp
				20					25					30
Pro	Pro	Ala	Val	Leu	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro
				35					40					45
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu
				50					55					60
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys
				65					70					75
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro
				80					85					90
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu
				95					100					105
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly
				110					115					120
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln
				125					130					135
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His
				140					145					150
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys
				155					160					165
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro

	170		175		180
Gly Leu Thr Pro	Arg Pro Val Pro Ser	Leu Pro Cys Asn Val Thr			
	185	190			195
Leu Glu Asp Phe	Tyr Gly Val Phe Ser	Ser Pro Gly Tyr Thr His			
	200	205			210
Leu Ala Ser Val	Ser His Pro Gln Ser	Cys His Trp Leu Leu Asp			
	215	220			225
Pro His Asp Gly	Arg Arg Leu Ala Val	Arg Phe Thr Ala Leu Asp			
	230	235			240
Leu Gly Phe Gly	Asp Ala Val His Val	Tyr Asp Gly Pro Gly Pro			
	245	250			255
Pro Glu Ser Ser	Arg Leu Leu Arg Ser	Leu Thr His Phe Ser Asn			
	260	265			270
Gly Lys Ala Val	Thr Val Glu Thr Leu	Ser Gly Gln Ala Val Val			
	275	280			285
Ser Tyr His Thr	Val Ala Trp Ser Asn	Gly Arg Gly Phe Asn Ala			
	290	295			300
Thr Tyr His Val	Arg Gly Tyr Cys Leu	Pro Trp Asp Arg Pro Cys			
	305	310			315
Gly Leu Gly Ser	Gly Leu Gly Ala Gly	Glu Gly Leu Gly Glu Arg			
	320	325			330
Cys Tyr Ser Glu	Ala Gln Arg Cys Asp	Gly Ser Trp Asp Cys Ala			
	335	340			345
Asp Gly Thr Asp	Glu Glu Asp Cys Pro	Gly Cys Pro Pro Gly His			
	350	355			360
Phe Pro Cys Gly	Ala Ala Gly Thr Ser	Gly Ala Thr Ala Cys Tyr			
	365	370			375
Leu Pro Ala Asp	Arg Cys Asn Tyr Gln	Thr Phe Cys Ala Asp Gly			
	380	385			390
Ala Asp Glu Arg	Arg Cys Arg His Cys	Gln Pro Gly Asn Phe Arg			
	395	400			405
Cys Arg Asp Glu	Lys Cys Val Tyr Glu	Thr Trp Val Cys Asp Gly			
	410	415			420
Gln Pro Asp Cys	Ala Asp Gly Ser Asp	Glu Trp Asp Cys Ser Tyr			
	425	430			435
Val Leu Pro Arg	Lys Val Ile Thr Ala	Ala Val Ile Gly Ser Leu			
	440	445			450
Val Cys Gly Leu	Leu Leu Val Ile Ala	Leu Gly Cys Thr Cys Lys			
	455	460			465

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 aaaaaaaaaa aaa 663

<210> 190

<211> 152

<212> PRT

<213> Homo sapiens

<400> 190

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe
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Ser	Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Ala	Leu	Thr	Val
				20					25					30
Thr	Ser	Met	Thr	Phe	Phe	Ile	Ile	Ala	Gln	Ala	Pro	Glu	Pro	Tyr
				35					40					45
Ile	Val	Ile	Thr	Gly	Phe	Glu	Val	Thr	Val	Ile	Leu	Phe	Phe	Ile
				50					55					60
Leu	Leu	Tyr	Val	Leu	Arg	Leu	Asp	Arg	Leu	Met	Lys	Trp	Leu	Phe
				65					70					75
Trp	Pro	Leu	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe
				80					85					90
Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr
				95					100					105
Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys
				110					115					120
Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn
				125					130					135
Pro	Ser	Gly	Pro	Tyr	Gln	Lys	Lys	Pro	Val	His	Glu	Lys	Lys	Glu
				140					145					150

Val Leu

<210> 191
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 212, 234, 487
<223> unknown base

<400> 191
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ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100
ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150
catcgcccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200
ggcactaact gngacatcta tgaccttttt tatnatcgca caagcccctg 250
aacatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350
gcctttgctt gatattatca actcactggc aacaacagta ttcattgctca 400
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggc 450
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cgttttgcag aacctactca ggcag 25

<210> 193
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 193
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194
<211> 40

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 194
aaagtgtctgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195
<211> 1879
<212> DNA
<213> Homo sapien

<400> 195
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ggaccggcta ggctgggcgc gccccccggg ccccgccgtg ggcatgggacg 100
cactggccccg ggcgtgtctg ctgcctctgc tggcccagtg gtccttgccg 150
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 aaataattaa aaaaaaaact tcattctaa 1879

<210> 196
 <211> 518
 <212> PRT
 <213> Homo sapien

<400> 196
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 20 25 30
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 35 40 45
 Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu
 50 55 60
 Ala Leu Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala
 65 70 75
 Asn Phe Leu Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg
 80 85 90
 Gly Tyr Tyr Leu Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu
 95 100 105

Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly	
				110					115					120	
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser	
				125					130					135	
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr	
				140					145					150	
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile	
				155					160					165	
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile	
				170					175					180	
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly	
				185					190					195	
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser	
				200					205					210	
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro	
				215					220					225	
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala	
				230					235					240	
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu	
				245					250					255	
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu	
				260					265					270	
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly	
				275					280					285	
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala	
				290					295					300	
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val	
				305					310					315	
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro	
				320					325					330	
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp	
				335					340					345	
Thr	Asn	Ser	Glu	Thr	Pro	Trp	Ser	Tyr	Phe	Pro	Lys	Ile	Ser	Ile	
				350					355					360	
Tyr	Leu	Arg	Asp	Glu	Asn	Ser	Ser	Arg	Ser	Phe	Arg	Ile	Thr	Ile	
				365					370					375	
Leu	Pro	Gln	Leu	Tyr	Ile	Gln	Pro	Met	Met	Gly	Ala	Gly	Leu	Asn	
				380					385					390	
Tyr	Glu	Cys	Tyr	Arg	Phe	Gly	Ile	Ser	Pro	Ser	Thr	Asn	Ala	Leu	

	395		400		405
Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp					
	410		415		420
Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu					
	425		430		435
Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr					
	440		445		450
Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu					
	455		460		465
Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly					
	470		475		480
Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg					
	485		490		495
Cys Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser					
	500		505		510
Ser Leu Val Arg His Arg Trp Lys					
	515				

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<220>
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<210> 198
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 <212> DNA
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<220>
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<400> 198
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<220>
 <223> Synthetic oligonucleotide probe

<400> 199
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<210> 200
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 200
 gccttggtc gttctcttc 19

<210> 201
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 201
 ggtcctgtgc ctggatgg 18

<210> 202
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 202
 gacaagacta cctccgttgg tc 22

<210> 203
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 203
 tgatgcacag ttcagcacct gttg 24

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 <212> DNA
 <213> Artificial Sequence

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<210> 205
 <211> 1939
 <212> DNA

<213> Homo sapiens

<400> 205

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gggcgggagc cgggaggcgc ggccggcatg gaggcgctgc tgctgggcgc 150
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 aattaccccc atgttaatga agcggaatta ggctcccgag ctaagggact 1700
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 cagggcaggg cagctggtat cgaggtgccc catgggagta aggggacgcc 1850
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 taaagcgcgt tgaccgccaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206
 <211> 377
 <212> PRT
 <213> Homo sapiens

<400> 206
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 Val Leu Val Tyr Tyr Asn Leu Val Lys Ala Pro Pro Cys Gly Gly
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 Met Gly Asn Leu Arg Gly Arg Thr Ala Val Val Thr Gly Ala Asn
 35 40 45
 Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly
 50 55 60
 Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala
 65 70 75
 Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile
 80 85 90
 Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe
 95 100 105
 Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile
 110 115 120
 His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe
 125 130 135
 Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr
 140 145 150

His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val	
				155					160					165	
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe	
				170					175					180	
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg	
				185					190					195	
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu	
				200					205					210	
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala	
				215					220					225	
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro	
				230					235					240	
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu	
				245					250					255	
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu	
				260					265					270	
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys	
				275					280					285	
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala	
				290					295					300	
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro	
				305					310					315	
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser	
				320					325					330	
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr	
				335					340					345	
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser	
				350					355					360	
Lys	Met	Thr	His	Arg	Ile	Gln	Ala	Lys	Val	Glu	Pro	Glu	Ile	Gln	
				365					370					375	

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

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<223> Synthetic oligonucleotide probe

<400> 208
acgccagtgg cctcaagctg gttg 24

<210> 209
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<223> Synthetic oligonucleotide probe

<400> 209
ctttctgagc tctgagccac ggttggacat cctcatccac aatgc 45

<210> 210
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<212> DNA
<213> Homo sapiens

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caagcctcag gccagccacc tcccaccatc cgctgggttg tgaatgggca 200
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 <212> PRT
 <213> Homo sapiens
 <400> 211
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 20 25 30
 Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu
 35 40 45
 Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His His Leu
 50 55 60
 Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Arg Gly
 65 70 75
 His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr
 80 85 90
 Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly
 95 100 105
 Ala Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln
 110 115 120
 Pro Arg Asp Met Val Ala Val Val Gly Glu Gln Phe Thr Leu Glu
 125 130 135
 Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp
 140 145 150
 Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val
 155 160 165
 Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu
 170 175 180
 Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu
 185 190 195
 Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr
 200 205 210
 Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val
 215 220 225
 Thr Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro
 230 235 240

Ala	Val	Trp	Leu	Ser	Trp	Lys	Val	Ser	Gly	Pro	Ala	Ala	Pro	Ala	
				245					250					255	
Gln	Ser	Tyr	Thr	Ala	Leu	Phe	Arg	Thr	Gln	Thr	Ala	Pro	Gly	Gly	
				260					265					270	
Gln	Gly	Ala	Pro	Trp	Ala	Glu	Glu	Leu	Leu	Ala	Gly	Trp	Gln	Ser	
				275					280					285	
Ala	Glu	Leu	Gly	Gly	Leu	His	Trp	Gly	Gln	Asp	Tyr	Glu	Phe	Lys	
				290					295					300	
Val	Arg	Pro	Ser	Ser	Gly	Arg	Ala	Arg	Gly	Pro	Asp	Ser	Asn	Val	
				305					310					315	
Leu	Leu	Leu	Arg	Leu	Pro	Glu	Lys	Val	Pro	Ser	Ala	Pro	Pro	Gln	
				320					325					330	
Glu	Val	Thr	Leu	Lys	Pro	Gly	Asn	Gly	Thr	Val	Phe	Val	Ser	Trp	
				335					340					345	
Val	Pro	Pro	Pro	Ala	Glu	Asn	His	Asn	Gly	Ile	Ile	Arg	Gly	Tyr	
				350					355					360	
Gln	Val	Trp	Ser	Leu	Gly	Asn	Thr	Ser	Leu	Pro	Pro	Ala	Asn	Trp	
				365					370					375	
Thr	Val	Val	Gly	Glu	Gln	Thr	Gln	Leu	Glu	Ile	Ala	Thr	His	Met	
				380					385					390	
Pro	Gly	Ser	Tyr	Cys	Val	Gln	Val	Ala	Ala	Val	Thr	Gly	Ala	Gly	
				395					400					405	
Ala	Gly	Glu	Pro	Ser	Arg	Pro	Val	Cys	Leu	Leu	Leu	Glu	Gln	Ala	
				410					415					420	
Met	Glu	Arg	Ala	Thr	Gln	Glu	Pro	Ser	Glu	His	Gly	Pro	Trp	Thr	
				425					430					435	
Leu	Glu	Gln	Leu	Arg	Ala	Thr	Leu	Lys	Arg	Pro	Glu	Val	Ile	Ala	
				440					445					450	
Thr	Cys	Gly	Val	Ala	Leu	Trp	Leu	Leu	Leu	Leu	Gly	Thr	Ala	Val	
				455					460					465	
Cys	Ile	His	Arg	Arg	Arg	Arg	Ala	Arg	Val	His	Leu	Gly	Pro	Gly	
				470					475					480	
Leu	Tyr	Arg	Tyr	Thr	Ser	Glu	Asp	Ala	Ile	Leu	Lys	His	Arg	Met	
				485					490					495	
Asp	His	Ser	Asp	Ser	Gln	Trp	Leu	Ala	Asp	Thr	Trp	Arg	Ser	Thr	
				500					505					510	
Ser	Gly	Ser	Arg	Asp	Leu	Ser	Ser	Ser	Ser	Ser	Leu	Ser	Ser	Arg	
				515					520					525	
Leu	Gly	Ala	Asp	Ala	Arg	Asp	Pro	Leu	Asp	Cys	Arg	Arg	Ser	Leu	

				530					535					540
Leu	Ser	Trp	Asp	Ser 545	Arg	Ser	Pro	Gly	Val 550	Pro	Leu	Leu	Pro	Asp 555
Thr	Ser	Thr	Phe	Tyr 560	Gly	Ser	Leu	Ile	Ala 565	Glu	Leu	Pro	Ser	Ser 570
Thr	Pro	Ala	Arg	Pro 575	Ser	Pro	Gln	Val	Pro 580	Ala	Val	Arg	Arg	Leu 585
Pro	Pro	Gln	Leu	Ala 590	Gln	Leu	Ser	Ser	Pro 595	Cys	Ser	Ser	Ser	Asp 600
Ser	Leu	Cys	Ser	Arg 605	Arg	Gly	Leu	Ser	Ser 610	Pro	Arg	Leu	Ser	Leu 615
Ala	Pro	Ala	Glu	Ala 620	Trp	Lys	Ala	Lys	Lys 625	Lys	Gln	Glu	Leu	Gln 630
His	Ala	Asn	Ser	Ser 635	Pro	Leu	Leu	Arg	Gly 640	Ser	His	Ser	Leu	Glu 645
Leu	Arg	Ala	Cys	Glu 650	Leu	Gly	Asn	Arg	Gly 655	Ser	Lys	Asn	Leu	Ser 660
Gln	Ser	Pro	Gly	Ala 665	Val	Pro	Gln	Ala	Leu 670	Val	Ala	Trp	Arg	Ala 675
Leu	Gly	Pro	Lys	Leu 680	Leu	Ser	Ser	Ser	Asn 685	Glu	Leu	Val	Thr	Arg 690
His	Leu	Pro	Pro	Ala 695	Pro	Leu	Phe	Pro	His 700	Glu	Thr	Pro	Pro	Thr 705
Gln	Ser	Gln	Gln	Thr 710	Gln	Pro	Pro	Val	Ala 715	Pro	Gln	Ala	Pro	Ser 720
Ser	Ile	Leu	Leu	Pro 725	Ala	Ala	Pro	Ile	Pro 730	Ile	Leu	Ser	Pro	Cys 735
Ser	Pro	Pro	Ser	Pro 740	Gln	Ala	Ser	Ser	Leu 745	Ser	Gly	Pro	Ser	Pro 750
Ala	Ser	Ser	Arg	Leu 755	Ser	Ser	Ser	Ser	Leu 760	Ser	Ser	Leu	Gly	Glu 765
Asp	Gln	Asp	Ser	Val 770	Leu	Thr	Pro	Glu	Glu 775	Val	Ala	Leu	Cys	Leu 780
Glu	Leu	Ser	Glu	Gly 785	Glu	Glu	Thr	Pro	Arg 790	Asn	Ser	Val	Ser	Pro 795
Met	Pro	Arg	Ala	Pro 800	Ser	Pro	Pro	Thr	Thr 805	Tyr	Gly	Tyr	Ile	Ser 810
Val	Pro	Thr	Ala	Ser 815	Glu	Phe	Thr	Asp	Met 820	Gly	Arg	Thr	Gly	Gly 825

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 215

<211> 2749

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1869, 1887

<223> unknown base

<400> 215

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gcgggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150

ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200

tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250

agggcaggggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtgggg 350

cgaaaaacgg ggccccgatg agtctttact gatctctctg ttcgtctttc 400

caggaccctg ctgtccctccc tccccttctc ccaccttcca gcctctggct 450

acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccagg 500

attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550

agacaggggc tgaggcccct ccattgccag ggacttccca gtacgggcac 600

gaaaggactt ctcagtacac aggaacctct cctcaccag cgacctctcc 650

tcctgcaggg agtcccgcc ccccatgca gctggactcc acctcagcag 700

aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750

atcccgatgg tccgcatact ggccccagtc ctggtgctgc tgagccttct 800

gtcagccgca ggctgatcg cttctgcag ccacctgctc ctgtggagaa 850

aggaagctca acaggccacg gagacacaga ggaacgagaa gttctggctc 900

tcacgcttga ctgcggagga aaaggaagcc ccttcccagg cccctgaggg 950

ggacgtgata tcgatgctc ccctccacac atctgaggag gagctgggct 1000

TOEFL® EBT®

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 tctttttaca gagcaattat cttgtatata caactttgta tcctgccttt 2650
 tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700
 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaa 2749

<210> 216
 <211> 332
 <212> PRT
 <213> Homo sapiens

<400> 216
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 1 5 10 15
 Tyr Glu Ala Leu Glu Gly Pro Glu Glu Ile Ser Gly Phe Glu Gly
 20 25 30
 Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp
 35 40 45
 His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg
 50 55 60
 Cys Ser Gly Thr Ile Tyr Ala Glu Glu Gly Gln Glu Thr Met
 65 70 75
 Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu
 80 85 90
 Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr
 95 100 105
 Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile
 110 115 120
 Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser
 125 130 135
 Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala
 140 145 150
 Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu
 155 160 165
 Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu
 170 175 180
 Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr
 185 190 195
 Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro

Ala	Gly	Ser	Ser	Arg	Pro	Pro	Met	Gln	Leu	Asp	Ser	Thr	Ser	Ala
				215					220					225
Glu	Asp	Thr	Ser	Pro	Ala	Leu	Ser	Ser	Gly	Ser	Ser	Lys	Pro	Arg
				230					235					240
Val	Ser	Ile	Pro	Met	Val	Arg	Ile	Leu	Ala	Pro	Val	Leu	Val	Leu
				245					250					255
Leu	Ser	Leu	Leu	Ser	Ala	Ala	Gly	Leu	Ile	Ala	Phe	Cys	Ser	His
				260					265					270
Leu	Leu	Leu	Trp	Arg	Lys	Glu	Ala	Gln	Gln	Ala	Thr	Glu	Thr	Gln
				275					280					285
Arg	Asn	Glu	Lys	Phe	Trp	Leu	Ser	Arg	Leu	Thr	Ala	Glu	Glu	Lys
				290					295					300
Glu	Ala	Pro	Ser	Gln	Ala	Pro	Glu	Gly	Asp	Val	Ile	Ser	Met	Pro
				305					310					315
Pro	Leu	His	Thr	Ser	Glu	Glu	Glu	Leu	Gly	Phe	Ser	Lys	Phe	Val
				320					325					330

Ser Ala

- <210> 217
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 217
- ccctgcagtg cacctacagg gaag 24
- <210> 218
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 218
- ctgtcttccc ctgcttggt gtgg 24
- <210> 219
- <211> 47
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe

<400> 219
 ggtgcaggaa ggggtgggatc ctcttctctc gctgctctgg ccacatc 47

<210> 220
 <211> 950
 <212> DNA
 <213> Homo sapiens

<400> 220
 ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50
 ggggtggcag gagccgcaga gccagagcag acagccgaga aacagggtga 100
 cagtgtgaaa gaaccagtgg tctcgctctg ttgccaggc tagagtgtac 150
 tggcgtgatc atagctcact gcagcctcag actcctggac ttgagaaatc 200
 ctctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250
 cctgtttctt ctcttctgt gagtggacca cggaggctgg tgagctgcct 300
 gtcatcccaa agctcagctc tgagccagag tgggtggtggc tccacctctg 350
 ccgccggcat agaagccagg agcagggtc tcagaaggcg gtggtgcca 400
 gctgggatca tgttgttggc cctggtctgt ctgctcagct gcctgctacc 450
 ctccagttag gccaaagctct acggtcgttg tgaactggcc agagtgtac 500
 atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550
 tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600
 ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650
 ggtgcagcaa cctcaacctg aacgtcccca acgtgtgccg gatgtactgc 700
 tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750
 gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800
 actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850
 gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900
 cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 221
 Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser
 1 5 10 15
 Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu
 20 25 30

<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225

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gtgcctgctg tgcgtgcgcc tcctcgtctt cgccgtcttc tcagccgccg 100
cgagcaactg gctgtacctg gccaaactgt cgtcggtggg gagcatctca 150
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200
gatgtgcaag cggaacctgg aagtcattga ctcggtgcgc cgcggtgccc 250
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300
tgctccacac tcgactcctt gcccgctctt ggcaaggtgg tgacgcaagg 350
gactcgggag gcggccttcg tgtacgcat ctcttcggca ggtgtggcct 400
ttgcagtgc gcgggcgtgc agcagtgggg agctggagaa gtgcggctgt 450
gacaggacag tgcattgggt cagcccacag ggcttcaggt ggtcaggatg 500
ctctgacaac atcgccctac gtgtggcctt ctacagtcg tttgtggatg 550
tgccgggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600
cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650
atgcaagtgc cacggggtgt caggctcctg tgaggtaaag acgtgctggc 700
gagccgtgcc gcccttcgc cagggtgggt acgcactgaa ggagaagttt 750
gatggtgcca ctgagggtga gccacgcgc gtgggctcct ccagggcact 800
ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850
acttgagacc tagccccgac ttctgtgagc aggacatgcg cagcggcgtg 900
ctgggcacga ggggccgcac atgcaacaag acgtccaagg ccatcgacgg 950
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aaacagtctc ccaccacctc cccaagaga tactggttgt attttttgtt 1200
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gctgccactg accactcagt tggtatctgt gtccgttttt ctacttgcag 1400
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 acacacacac ggacacacac acacacctgc gagagagagg gaggaagg 2000
 ctgtgccttt gcagtcacgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226

<211> 351

<212> PRT

<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe
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Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys
				20					25					30
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys
				35					40					45
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn
				50					55					60
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile
				65					70					75
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser
				80					85					90
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly
				95					100					105
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val
				110					115					120

Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys
				125					130					135
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe
				140					145					150
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe
				155					160					165
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser
				170					175					180
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg
				185					190					195
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly
				200					205					210
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro
				215					220					225
Pro	Phe	Arg	Gln	Val	Gly	His	Ala	Leu	Lys	Glu	Lys	Phe	Asp	Gly
				230					235					240
Ala	Thr	Glu	Val	Glu	Pro	Arg	Arg	Val	Gly	Ser	Ser	Arg	Ala	Leu
				245					250					255
Val	Pro	Arg	Asn	Ala	Gln	Phe	Lys	Pro	His	Thr	Asp	Glu	Asp	Leu
				260					265					270
Val	Tyr	Leu	Glu	Pro	Ser	Pro	Asp	Phe	Cys	Glu	Gln	Asp	Met	Arg
				275					280					285
Ser	Gly	Val	Leu	Gly	Thr	Arg	Gly	Arg	Thr	Cys	Asn	Lys	Thr	Ser
				290					295					300
Lys	Ala	Ile	Asp	Gly	Cys	Glu	Leu	Leu	Cys	Cys	Gly	Arg	Gly	Phe
				305					310					315
His	Thr	Ala	Gln	Val	Glu	Leu	Ala	Glu	Arg	Cys	Ser	Cys	Lys	Phe
				320					325					330
His	Trp	Cys	Cys	Phe	Val	Lys	Cys	Arg	Gln	Cys	Gln	Arg	Leu	Val
				335					340					345
Glu	Leu	His	Thr	Cys	Arg									
				350										

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 228
 tgggtgggaga ctgttttaaat tatcggcc 28

<210> 229
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 229
 tgcttcgtca agtgccggca gtgccagcgg ctcgtggagt t 41

<210> 230
 <211> 1355
 <212> DNA
 <213> Homo sapiens

<400> 230
 cggacgcgtg ggcggacgcg tgggaggacg cgtgggaggga cgcgtgggct 50
 ggggtgcctgc atogccatgg acaccaccag gtacagcaag tggggcggca 100
 gctccgagga ggtccccgga gggccctggg gacgctgggt gcaactggagc 150
 aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200
 ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gagcgcgcgg 250
 cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300
 gcggcgctgg gtgccctgaa ggaggaggct ggagactgcc acagctgctg 350
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 cgcgtgaccc agggcttggc tgaagccggc aggggcccgtg aggacgtccg 500
 cactgagctg ttccggggcg tggaggccgt gaggctccag aacaactcct 550
 gcgagccgtg cccacgctg tggctgtcct tcgagggctc ctgctacttt 600
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 tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggttcc 700
 tcaactcgaa cacgcgtggc cgtggttact ggctgggcct gagggctgtg 750

cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800
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agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900
gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950
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actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200
ctcctgcgtc cccgtgatat gcctccactt ctctccctaa ccaaggttag 1250
gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300
gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350
aaaaa 1355

<210> 231

<211> 293

<212> PRT

<213> Homo sapiens

<400> 231

Met	Asp	Thr	Thr	Arg	Tyr	Ser	Lys	Trp	Gly	Gly	Ser	Ser	Glu	Glu
1				5					10					15
Val	Pro	Gly	Gly	Pro	Trp	Gly	Arg	Trp	Val	His	Trp	Ser	Arg	Arg
				20					25					30
Pro	Leu	Phe	Leu	Ala	Leu	Ala	Val	Leu	Val	Thr	Thr	Val	Leu	Trp
				35					40					45
Ala	Val	Ile	Leu	Ser	Ile	Leu	Leu	Ser	Lys	Ala	Ser	Thr	Glu	Arg
				50					55					60
Ala	Ala	Leu	Leu	Asp	Gly	His	Asp	Leu	Leu	Arg	Thr	Asn	Ala	Ser
				65					70					75
Lys	Gln	Thr	Ala	Ala	Leu	Gly	Ala	Leu	Lys	Glu	Glu	Val	Gly	Asp
				80					85					90
Cys	His	Ser	Cys	Cys	Ser	Gly	Thr	Gln	Ala	Gln	Leu	Gln	Thr	Thr
				95					100					105
Arg	Ala	Glu	Leu	Gly	Glu	Ala	Gln	Ala	Lys	Leu	Met	Glu	Gln	Glu
				110					115					120
Ser	Ala	Leu	Arg	Glu	Leu	Arg	Glu	Arg	Val	Thr	Gln	Gly	Leu	Ala
				125					130					135

Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg	
				140					145					150	
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys	
				155					160					165	
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	
				170					175					180	
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp	
				185					190					195	
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly	
				200					205					210	
Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu	
				215					220					225	
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val	
				230					235					240	
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro	
				245					250					255	
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr	
				260					265					270	
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp	
				275					280					285	
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys								
				290											

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgtcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gagggatgc cgacccgggg aaggtcgctg ggcagggcga 50
gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctctctcttt 100
ctccacgctc ctatctgcct ctcgctggag gccaggcctg gcagcatcga 150
agacaggagg aactggagcc tcattggccg gcccggggcg ccggcctcgg 200
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<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

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				20					25					30
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile
				35					40					45
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr
				50					55					60
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala
				65					70					75
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val
				80					85					90
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala
				95					100					105
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Leu	Gln	Ser	Val

110	115	120
His Glu Val Phe Ser Ala Pro Ala Val	Pro Ser Gly Thr Gly Gln	
125	130	135
Thr Ser Ala Glu Leu Glu Val Gln Arg	Arg His Ser Leu Val Ser	
140	145	150
Phe Val Val Arg Ile Val Pro Ser Pro	Asp Trp Phe Val Gly Val	
155	160	165
Asp Ser Leu Asp Leu Cys Asp Gly Asp	Arg Trp Arg Glu Gln Ala	
170	175	180
Ala Leu Asp Leu Tyr Pro Tyr Asp Ala	Gly Thr Asp Ser Gly Phe	
185	190	195
Thr Phe Ser Ser Pro Asn Phe Ala Thr	Ile Pro Gln Asp Thr Val	
200	205	210
Thr Glu Ile Thr Ser Ser Ser Pro Ser	His Pro Ala Asn Ser Phe	
215	220	225
Tyr Tyr Pro Arg Leu Lys Ala Leu Pro	Pro Ile Ala Arg Val Thr	
230	235	240
Leu Leu Arg Leu Arg Gln Ser Pro Arg	Ala Phe Ile Pro Pro Ala	
245	250	255
Pro Val Leu Pro Ser Arg Asp Asn Glu	Ile Val Asp Ser Ala Ser	
260	265	270
Val Pro Glu Thr Pro Leu Asp Cys Glu	Val Ser Leu Trp Ser Ser	
275	280	285
Trp Gly Leu Cys Gly Gly His Cys Gly	Arg Leu Gly Thr Lys Ser	
290	295	300
Arg Thr Arg Tyr Val Arg Val Gln Pro	Ala Asn Asn Gly Ser Pro	
305	310	315
Cys Pro Glu Leu Glu Glu Glu Ala Glu	Cys Val Pro Asp Asn Cys	
320	325	330

Val

<210> 237
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 237
 cagcaactgcc aggggaagag gg 22

<210> 238
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 238
 caggactcgc tacgtccg 18

 <210> 239
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 239
 cagccccttc tcctcctttc tccc 24

 <210> 240
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 240
 gcagttatca gggacgcact cagcc 25

 <210> 241
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 241
 ccagcgagag gcagatag 18

 <210> 242
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 242
 cggtcaccgt gtcctgcggt atg 23

 <210> 243
 <211> 42
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 243

cagccccttc tcctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

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aggaagagtg tactcgtagg cggacagctt tagtggccgg ccggccgctc 150
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagcttg 300
cagaaatfff atccaactff gtttgggaagc ttattatgac aataccatff 350
ttcatagagt tgtgcctggt ttcatagtcc aaggcggaga tcctactggc 400
acagggagtg gtggagagtc tatctatgga gcgccattca aagatgaatt 450
tcattcacgg ttgcgtffta atcggagagg actggttgcc atggcaaattg 500
ctggttctca tgataatggc agccagttff tcttcacact gggtcgagca 550
gatgaactta acaataagca taccatctff ggaaaggffa caggggatac 600
agtatataac atgttgcgac tgtcagaagt agacattgat gatgacgaaa 650
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tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaaacc 750
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tactfftcatt tggagaggaa gctgaggaag aagaggagga agtaaatcga 850
gttagtcaga gcatgaaggg caaaagcaaa agtagtcatt acttgcttaa 900
ggatgatcca catctcagtt ctgttccagt tgtagaaagt gaaaaagggtg 950
atgcaccaga tttagttgat gatggagaag atgaaagtgc agagcatgat 1000
gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgccaa 1050
aaaattaaaa aaggacacaa gtgcgaatgt taaatcagct ggagaaggag 1100

aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150
agacaattaa aacgggaact cttagcagca aaacaaaaaa aagtagaaaa 1200
tgcagcaaaa caagcagaaa aaagaagtga agaggaagaa gcccctccag 1250
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tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggta 1800
catgtgtttt ttcctagctg accttttata ttgctaaatc tgaaataaaa 1850
taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245

<211> 472

<212> PRT

<213> Homo sapiens

<400> 245

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Leu	Leu	Lys	Thr	Thr	Ala	Gly	Asp	Ile	Asp	Ile	Glu	Leu	Trp	Ser
			20						25					30
Lys	Glu	Ala	Pro	Lys	Ala	Cys	Arg	Asn	Phe	Ile	Gln	Leu	Cys	Leu
			35						40					45
Glu	Ala	Tyr	Tyr	Asp	Asn	Thr	Ile	Phe	His	Arg	Val	Val	Pro	Gly
			50						55					60
Phe	Ile	Val	Gln	Gly	Gly	Asp	Pro	Thr	Gly	Thr	Gly	Ser	Gly	Gly
			65						70					75
Glu	Ser	Ile	Tyr	Gly	Ala	Pro	Phe	Lys	Asp	Glu	Phe	His	Ser	Arg
			80						85					90
Leu	Arg	Phe	Asn	Arg	Arg	Gly	Leu	Val	Ala	Met	Ala	Asn	Ala	Gly
			95						100					105

Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala	
				110					115					120	
Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly	
				125					130					135	
Asp	Thr	Val	Tyr	Asn	Met	Leu	Arg	Leu	Ser	Glu	Val	Asp	Ile	Asp	
				140					145					150	
Asp	Asp	Glu	Arg	Pro	His	Asn	Pro	His	Lys	Ile	Lys	Ser	Cys	Glu	
				155					160					165	
Val	Leu	Phe	Asn	Pro	Phe	Asp	Asp	Ile	Ile	Pro	Arg	Glu	Ile	Lys	
				170					175					180	
Arg	Leu	Lys	Lys	Glu	Lys	Pro	Glu	Glu	Glu	Val	Lys	Lys	Leu	Lys	
				185					190					195	
Pro	Lys	Gly	Thr	Lys	Asn	Phe	Ser	Leu	Leu	Ser	Phe	Gly	Glu	Glu	
				200					205					210	
Ala	Glu	Glu	Glu	Glu	Glu	Glu	Val	Asn	Arg	Val	Ser	Gln	Ser	Met	
				215					220					225	
Lys	Gly	Lys	Ser	Lys	Ser	Ser	His	Asp	Leu	Leu	Lys	Asp	Asp	Pro	
				230					235					240	
His	Leu	Ser	Ser	Val	Pro	Val	Val	Glu	Ser	Glu	Lys	Gly	Asp	Ala	
				245					250					255	
Pro	Asp	Leu	Val	Asp	Asp	Gly	Glu	Asp	Glu	Ser	Ala	Glu	His	Asp	
				260					265					270	
Glu	Tyr	Ile	Asp	Gly	Asp	Glu	Lys	Asn	Leu	Met	Arg	Glu	Arg	Ile	
				275					280					285	
Ala	Lys	Lys	Leu	Lys	Lys	Asp	Thr	Ser	Ala	Asn	Val	Lys	Ser	Ala	
				290					295					300	
Gly	Glu	Gly	Glu	Val	Glu	Lys	Lys	Ser	Val	Ser	Arg	Ser	Glu	Glu	
				305					310					315	
Leu	Arg	Lys	Glu	Ala	Arg	Gln	Leu	Lys	Arg	Glu	Leu	Leu	Ala	Ala	
				320					325					330	
Lys	Gln	Lys	Lys	Val	Glu	Asn	Ala	Ala	Lys	Gln	Ala	Glu	Lys	Arg	
				335					340					345	
Ser	Glu	Glu	Glu	Glu	Ala	Pro	Pro	Asp	Gly	Ala	Val	Ala	Glu	Tyr	
				350					355					360	
Arg	Arg	Glu	Lys	Gln	Lys	Tyr	Glu	Ala	Leu	Arg	Lys	Gln	Gln	Ser	
				365					370					375	
Lys	Lys	Gly	Thr	Ser	Arg	Glu	Asp	Gln	Thr	Leu	Ala	Leu	Leu	Asn	
				380					385					390	
Gln	Phe	Lys	Ser	Lys	Leu	Thr	Gln	Ala	Ile	Ala	Glu	Thr	Pro	Glu	

395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met		
410	415	420
Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp		
425	430	435
Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg		
440	445	450
Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met		
455	460	465
Arg Glu Lys Lys Glu Arg Arg		
470		

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tgttgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249
caactggaac aggaactgag atgtggatc 29

<210> 250
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 250
ctgggtcagc agtgcaaggg tctg 24

<210> 251
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 251
cctctccgat taaaacgc 18

<210> 252
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 252
gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253
<211> 2456
<212> DNA
<213> Homo sapiens

<400> 253
cgccgccgtt ggggctggaa gttcccgccca ggtccgtgcc gggcgagaga 50
gatgctgccc ggcccgcctc ggctttgagg cgagagaagt gtcccagacc 100
catttcgcct tgctgacggc gtcgagccct ggccagacat gtccacaggg 150
ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgccggcgg 200
gaccagcaca ggcggcggttt tctccttcgg aacgggaacg tctagcaacc 250
cttctgtggg gctcaatatt ggaaatcttg gaagtacttc aactccagca 300
actacatctg ctctttcaag tggttttgga accgggctct ttggatctaa 350
acctgccact ggggttcactc taggaggaac aaatacagggt gccttgca 400

ccaagaggcc tcaagtggtc accaaatatg gaaccctgca aggaaaacag 450
atgcatgtgg ggaagacacc catccaagtc tttttaggag tccccttctc 500
cagacctcct ctaggtatcc tcaggttttgc acctccagaa cccccggagc 550
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agatgctacg aaaccgtatg atggacatag ttcaagatgc cactttcgtg 1650
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aatctgcct gctggccacg ctacaacaag gatgaaaagt acctgcagct 1750
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cagggcctgg ggagactagc catggacata cctgggggaca agagttctac 1950
ccacccagct ttagaactgc aggagctccc tgctgcctcc aggccaaagc 2000
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gtctatacac aggggtggtc tcttcaataa agaagtgttg attagaaaaa 2450
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<210> 254

<211> 545

<212> PRT

<213> Homo sapiens

<400> 254

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				20					25					30
Gly	Thr	Gly	Thr	Ser	Ser	Asn	Pro	Ser	Val	Gly	Leu	Asn	Phe	Gly
				35					40					45
Asn	Leu	Gly	Ser	Thr	Ser	Thr	Pro	Ala	Thr	Thr	Ser	Ala	Pro	Ser
				50					55					60
Ser	Gly	Phe	Gly	Thr	Gly	Leu	Phe	Gly	Ser	Lys	Pro	Ala	Thr	Gly
				65					70					75
Phe	Thr	Leu	Gly	Gly	Thr	Asn	Thr	Gly	Ala	Leu	His	Thr	Lys	Arg
				80					85					90
Pro	Gln	Val	Val	Thr	Lys	Tyr	Gly	Thr	Leu	Gln	Gly	Lys	Gln	Met
				95					100					105
His	Val	Gly	Lys	Thr	Pro	Ile	Gln	Val	Phe	Leu	Gly	Val	Pro	Phe
				110					115					120
Ser	Arg	Pro	Pro	Leu	Gly	Ile	Leu	Arg	Phe	Ala	Pro	Pro	Glu	Pro
				125					130					135

Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro	
				140					145					150	
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	
				155					160					165	
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	
				170					175					180	
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	
				185					190					195	
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	
				200					205					210	
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	
				215					220					225	
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	
				230					235					240	
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	
				245					250					255	
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	
				260					265					270	
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	
				275					280					285	
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	
				290					295					300	
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	
				305					310					315	
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	
				320					325					330	
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	
				335					340					345	
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	
				350					355					360	
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	
				365					370					375	
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	
				380					385					390	
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	
				395					400					405	
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	
				410					415					420	
Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro	Asp	Asp	Pro	

425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val	Ser Ser Val Pro Tyr Leu	
440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn	Trp Leu Leu Pro Tyr Asn	
455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val	Val Glu Glu Tyr Leu Asp	
470	475	480
Asn Val Asn Glu His Asp Trp Lys Met	Leu Arg Asn Arg Met Met	
485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val	Tyr Ala Thr Leu Gln Thr	
500	505	510
Ala His Tyr His Arg Glu Thr Pro Met	Met Gly Ile Cys Pro Ala	
515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser	Thr Cys Ser Trp Ile Leu	
530	535	540
Pro Gln Glu Trp Ala		
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 256
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 256
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<210> 257
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 257
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<210> 258
<211> 2764
<212> DNA
<213> Homo sapiens

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actgccactg ctgctgtcct cgtgctggg cgggtcccag gctatggatg 100
ggagattctg gatacgagtg caggagtcat tgatggtgcc ggagggcctg 150
tgcatctctg tgccctgctc tttctcctac ccccgacaag actggacagg 200
gtctaccca gcttatggct actggttcaa agcagtgact gagacaacca 250
agggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300
acccggggcc gattccagct cactggggat cccgccaagg ggaactgctc 350
cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttctttc 400
gggtggagag aggaagctat gtgacatata atttcatgaa cgatgggttc 450
tttctaaaag taacagtgtc cagcttcacg cccagacccc aggaccacaa 500
caccgacctc acctgccatg tggacttctc cagaaagggg gtgagcgcac 550
agaggaccgt ccgactccgt gtggcctatg ccccagaga ccttgttatc 600
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 cccagcactt tgggaggcta aggtgggtgg attgcttgag cccaggagtt 2200
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 tttaaaccag agcaactcca tctggaatag gagctgaata aaatgaggct 2350
 gagacctact gggctgcatt ctcagacagt ggaggcattc taagtcacag 2400
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 gccacgagag tgacctctgg tgcctctcac tgctacactc ctgacagcac 2550
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tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

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Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met
				20					25					30
Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp
				50					55					60
Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr
				65					70					75
Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe
				80					85					90
Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile
				95					100					105
Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val
				110					115					120
Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe
				125					130					135
Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp
				140					145					150
His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly
				155					160					165
Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro
				170					175					180
Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu
				185					190					195
Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys
				200					205					210
Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro
				215					220					225
Ala	Thr	Leu	Ser	Trp	Val	Leu	Gln	Asn	Arg	Val	Leu	Ser	Ser	Ser
				230					235					240
His	Pro	Trp	Gly	Pro	Arg	Pro	Leu	Gly	Leu	Glu	Leu	Pro	Gly	Val
				245					250					255

Lys	Ala	Gly	Asp	Ser	Gly	Arg	Tyr	Thr	Cys	Arg	Ala	Glu	Asn	Arg	
				260					265					270	
Leu	Gly	Ser	Gln	Gln	Arg	Ala	Leu	Asp	Leu	Ser	Val	Gln	Tyr	Pro	
				275					280					285	
Pro	Glu	Asn	Leu	Arg	Val	Met	Val	Ser	Gln	Ala	Asn	Arg	Thr	Val	
				290					295					300	
Leu	Glu	Asn	Leu	Gly	Asn	Gly	Thr	Ser	Leu	Pro	Val	Leu	Glu	Gly	
				305					310					315	
Gln	Ser	Leu	Cys	Leu	Val	Cys	Val	Thr	His	Ser	Ser	Pro	Pro	Ala	
				320					325					330	
Arg	Leu	Ser	Trp	Thr	Gln	Arg	Gly	Gln	Val	Leu	Ser	Pro	Ser	Gln	
				335					340					345	
Pro	Ser	Asp	Pro	Gly	Val	Leu	Glu	Leu	Pro	Arg	Val	Gln	Val	Glu	
				350					355					360	
His	Glu	Gly	Glu	Phe	Thr	Cys	His	Ala	Arg	His	Pro	Leu	Gly	Ser	
				365					370					375	
Gln	His	Val	Ser	Leu	Ser	Leu	Ser	Val	His	Tyr	Lys	Lys	Gly	Leu	
				380					385					390	
Ile	Ser	Thr	Ala	Phe	Ser	Asn	Gly	Ala	Phe	Leu	Gly	Ile	Gly	Ile	
				395					400					405	
Thr	Ala	Leu	Leu	Phe	Leu	Cys	Leu	Ala	Leu	Ile	Ile	Met	Lys	Ile	
				410					415					420	
Leu	Pro	Lys	Arg	Arg	Thr	Gln	Thr	Glu	Thr	Pro	Arg	Pro	Arg	Phe	
				425					430					435	
Ser	Arg	His	Ser	Thr	Ile	Leu	Asp	Tyr	Ile	Asn	Val	Val	Pro	Thr	
				440					445					450	
Ala	Gly	Pro	Leu	Ala	Gln	Lys	Arg	Asn	Gln	Lys	Ala	Thr	Pro	Asn	
				455					460					465	
Ser	Pro	Arg	Thr	Pro	Pro	Pro	Pro	Gly	Ala	Pro	Ser	Pro	Glu	Ser	
				470					475					480	
Lys	Lys	Asn	Gln	Lys	Lys	Gln	Tyr	Gln	Leu	Pro	Ser	Phe	Pro	Glu	
				485					490					495	
Pro	Lys	Ser	Ser	Thr	Gln	Ala	Pro	Glu	Ser	Gln	Glu	Ser	Gln	Glu	
				500					505					510	
Glu	Leu	His	Tyr	Ala	Thr	Leu	Asn	Phe	Pro	Gly	Val	Arg	Pro	Arg	
				515					520					525	
Pro	Glu	Ala	Arg	Met	Pro	Lys	Gly	Thr	Gln	Ala	Asp	Tyr	Ala	Glu	
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<210> 260
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 260
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<210> 261
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 261
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<210> 262
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 262
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<210> 263
<211> 2857
<212> DNA
<213> Homo sapiens

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    caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150
    ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200
    aatgaatacg actagtcatc acatcggcca gctaagatct gatttagaca 250
    atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300
    acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350
    tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400
    tcgctactgg aagggtgtg gaacctgagt ctgagtttgt catcaaagtt 450

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<210> 264
 <211> 772
 <212> PRT
 <213> Homo sapiens

<400> 264
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 Leu Trp Pro Cys Leu Gly Ala Thr Glu Asn Ser Gln Thr Lys Lys
 20 25 30
 Val Lys Gln Pro Val Arg Ser His Leu Arg Val Lys Arg Gly Trp
 35 40 45
 Val Trp Asn Gln Phe Phe Val Pro Glu Glu Met Asn Thr Thr Ser
 50 55 60

His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn	
				65					70					75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe	
				80					85					90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu	
				95					100					105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile	
				110					115					120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val	
				125					130					135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp	
				140					145					150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr	
				155					160					165	
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser	
				170					175					180	
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro	
				185					190					195	
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser	
				200					205					210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln	
				215					220					225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr	
				230					235					240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile	
				245					250					255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro	
				260					265					270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile	
				275					280					285	
Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser	
				290					295					300	
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile	
				305					310					315	
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr	
				320					325					330	
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu	
				335					340					345	
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln	

				350					355					360
Val	Glu	Asp	Val	Asp 365	Glu	Pro	Pro	Leu	Phe 370	Leu	Leu	Pro	Tyr	Tyr 375
Val	Phe	Glu	Val	Phe 380	Glu	Glu	Thr	Pro	Gln 385	Gly	Ser	Phe	Val	Gly 390
Val	Val	Ser	Ala	Thr 395	Asp	Pro	Asp	Asn	Arg 400	Lys	Ser	Pro	Ile	Arg 405
Tyr	Ser	Ile	Thr	Arg 410	Ser	Lys	Val	Phe	Asn 415	Ile	Asn	Asp	Asn	Gly 420
Thr	Ile	Thr	Thr	Ser 425	Asn	Ser	Leu	Asp	Arg 430	Glu	Ile	Ser	Ala	Trp 435
Tyr	Asn	Leu	Ser	Ile 440	Thr	Ala	Thr	Glu	Lys 445	Tyr	Asn	Ile	Glu	Gln 450
Ile	Ser	Ser	Ile	Pro 455	Leu	Tyr	Val	Gln	Val 460	Leu	Asn	Ile	Asn	Asp 465
His	Ala	Pro	Glu	Phe 470	Ser	Gln	Tyr	Tyr	Glu 475	Thr	Tyr	Val	Cys	Glu 480
Asn	Ala	Gly	Ser	Gly 485	Gln	Val	Ile	Gln	Thr 490	Ile	Ser	Ala	Val	Asp 495
Arg	Asp	Glu	Ser	Ile 500	Glu	Glu	His	His	Phe 505	Tyr	Phe	Asn	Leu	Ser 510
Val	Glu	Asp	Thr	Asn 515	Asn	Ser	Ser	Phe	Thr 520	Ile	Ile	Asp	Asn	Gln 525
Asp	Asn	Thr	Ala	Val 530	Ile	Leu	Thr	Asn	Arg 535	Thr	Gly	Phe	Asn	Leu 540
Gln	Glu	Glu	Pro	Val 545	Phe	Tyr	Ile	Ser	Ile 550	Leu	Ile	Ala	Asp	Asn 555
Gly	Ile	Pro	Ser	Leu 560	Thr	Ser	Thr	Asn	Thr 565	Leu	Thr	Ile	His	Val 570
Cys	Asp	Cys	Gly	Asp 575	Ser	Gly	Ser	Thr	Gln 580	Thr	Cys	Gln	Tyr	Gln 585
Glu	Leu	Val	Leu	Ser 590	Met	Gly	Phe	Lys	Thr 595	Glu	Val	Ile	Ile	Ala 600
Ile	Leu	Ile	Cys	Ile 605	Met	Ile	Ile	Phe	Gly 610	Phe	Ile	Phe	Leu	Thr 615
Leu	Gly	Leu	Lys	Gln 620	Arg	Arg	Lys	Gln	Ile 625	Leu	Phe	Pro	Glu	Lys 630
Ser	Glu	Asp	Phe	Arg 635	Glu	Asn	Ile	Phe	Gln 640	Tyr	Asp	Asp	Glu	Gly 645

Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	650	655	660
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	665	670	675
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	680	685	690
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	695	700	705
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	710	715	720
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	725	730	735
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	740	745	750
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	755	760	765
Ser	Ala	Val	Gln	Ser	Asn	Asn									770		

<210> 265
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 24, 60, 141, 226, 228, 249, 252
 <223> unknown base

<400> 265
 atttcaaggc cagccatatt tttntgttga accaacaaca ggagtcataa 50
 gaatattnn taaaatggat agagaactgc aagatgagta ttgggtaatc 100
 attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150
 aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200
 aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
 tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
 aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

ttgcaggctct ggctatttta gttgccacag catggtatgg caatagaatc 650
 gttcaagaat tctatgaccc tatgaccca gtcaatgcca ggtacgaatt 700
 tggtcaggct ctcttactg gctgggctgc tgcttctctc tgccttctgg 750
 gaggtgccct actttgctgt tcctgtcccc gaaaaacaac ctcttacca 800
 acaccaaggc cctatccaaa acctgcacct tccagcggga aagactacgt 850
 gtgacacaga ggcaaaagga gaaaatcatg ttgaaacaaa ccgaaaatgg 900
 acattgagat actatcatta acattaggac cttagaattt tgggtattgt 950
 aatctgaagt atggtattac aaaacaaaca aacaaacaaa aaacccatgt 1000
 gttaaaatac tcaagtctaa acatggctta atcttatttt atcttctttc 1050
 ctcaatatag gaggaagat tttccattt gtattactgc ttccattga 1100
 gtaatcatatc tcaaatgggg gaaggggtgc tccttaaata tatatagata 1150
 tgtatatata catgtttttc tattaataat agacagtaaa atactattct 1200
 cattatgttg atactagcat acttaaaata tctctaaaat aggtaaatgt 1250
 atttaattcc atattgatga agatgtttat tgggtatattt tctttttcgt 1300
 ccttatatac atatgtaaca gtcaaatatc atttactctt cttcattagc 1350
 tttgggtgcc tttgccacaa gacctagcct aatttaccac ggatgaattc 1400
 tttcaattct tcatgcgtgc ccttttcata tacttatttt attttttacc 1450
 ataactttat agcaacttga tcgttattaa gcccttattt gttttgtgtt 1500
 tcattggtct ctatctcctg aatctaacac atttcatagc ctacatttta 1550
 gtttctaaag ccaagaagaa tttattacaa atcagaactt tggaggcaaa 1600
 tctttctgca tgaccaaagt gataaattcc tgttgacctt cccacacaat 1650
 ccctgtactc tgacccatag cactcttgtt tgctttgaaa atatttgtcc 1700
 aattgagtag ctgcatgctg ttccccagc tgttgtaaca caactttatt 1750
 gattgaattt ttaagctact tattcatagt tttatatccc cctaaactac 1800
 ctttttgttc ccatttcctt aattgtattg ttttccaag tgtaattatc 1850
 atgcggttta tatcttccta ataagggtgt gtctgtttgt ctgaacaaag 1900
 tgctagactt tctggagtga taatctggtg acaaatattc tctctgtagc 1950
 tgtaagcaag tcaactaatc tttctacctc ttttttctat ctgccaaatt 2000
 gagataatga tacttaacca gttagaagag gtagtgtgaa tattaattag 2050

tttatattac tcttattctt tgaacatgaa ctatgcctat gtagtgtctt 2100
tatttgctca gctggctgag aactgaaga agtcactgaa caaacctac 2150
acacgtacct tcatgtgatt cactgccttc ctctctctac cagtctatctt 2200
ccactgaaca aaacctacac acataccttc atgtgggttca gtgccttcct 2250
ctctctacca gtctatttcc actgaacaaa acctacgcac ataccttcat 2300
gtggctcagt gccttcctct ctctaccagt ctatttccat tctttcagct 2350
gtgtctgaca tgtttggtgt ctgttccatt ttaacaactg ctcttacttt 2400
tccagtctgt acagaatgct atttcacttg agcaagatga tgtaatggaa 2450
aggggtgttg cactgggtgc tggagacctg gatttgagtc ttggtgctat 2500
caatcaccgt ctgtgtttga gcaaggcatt tggtgtgtgt aagcttattg 2550
cttcatctgt aagcgggtgt ttgtaattcc tgatcttccc acctcacagt 2600
gatgttggtg ggatccagtg agatagaata catgtaagtg tggttttgta 2650
atttaaaaag tgctatacta agggaaagaa ttgaggaatt aactgcatac 2700
gttttggtgt tgcttttcaa atgtttgaaa ataaaaaaaaa tgttaag 2747

<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

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1				5					10					15
Leu	Gly	Trp	Ile	Gly	Ala	Ile	Val	Ser	Thr	Ala	Leu	Pro	Gln	Trp
				20					25					30
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala
				35					40					45
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly
				50					55					60
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser
				65					70					75
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu
				80					85					90
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met
				95					100					105
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val
				110					115					120

Ile	Gly	Gly	Ala	Ile	Phe	Leu	Leu	Ala	Gly	Leu	Ala	Ile	Leu	Val
				125					130					135
Ala	Thr	Ala	Trp	Tyr	Gly	Asn	Arg	Ile	Val	Gln	Glu	Phe	Tyr	Asp
				140					145					150
Pro	Met	Thr	Pro	Val	Asn	Ala	Arg	Tyr	Glu	Phe	Gly	Gln	Ala	Leu
				155					160					165
Phe	Thr	Gly	Trp	Ala	Ala	Ala	Ser	Leu	Cys	Leu	Leu	Gly	Gly	Ala
				170					175					180
Leu	Leu	Cys	Cys	Ser	Cys	Pro	Arg	Lys	Thr	Thr	Ser	Tyr	Pro	Thr
				185					190					195
Pro	Arg	Pro	Tyr	Pro	Lys	Pro	Ala	Pro	Ser	Ser	Gly	Lys	Asp	Tyr
				200					205					210

Val

<210> 271
 <211> 564
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> unsure
 <222> 21, 69, 163, 434, 436, 444
 <223> unknown base

<400> 271
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 ggatggatcg ggcgcattc cactgccc ttcccagtg gaggatttta 100
 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150
 ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250
 tgatgggtgt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300
 gttggcatga agtgtatgaa gtgcttggaa gacgatgagg tgcagaagat 350
 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400
 ttttagttgc cacagcatgg tatggcaata gaancnttca acanttttat 450
 gaccctatga cccagtc aa tgccaggtag gaatttggtc aggctctctt 500
 cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550
 gctgttcctg tccc 564

<210> 272
 <211> 498

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341
<223> unknown base

<400> 272
acccttgacc caacgoggcc ccccgaccgn ttcattggcca aacgcgggnc 50
tccagctggt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100
cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150
acatcgtgac cggccaggcc ntgtacgagg ggctgtggat gtcttgctg 200
tcgcagagca ccgggcagat ccagtgcata gtctttgact cccttgctga 250
atctgagcag cacattgcaa gcaaccctg ccttgatggt ggttggcatc 300
ctcctgggag tgatagcaat cttnttggcc accgttgtnn ntgaagtgt 350
tgaagtgtt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400
gggggcgcca tatttcttct tgcaggtctg gctattttag ttgccacagc 450
atggtatggc aatagaatcg ttcaagaatt ctatgacct atgaccga 498

<210> 273
<211> 552
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394
<223> unknown base

<400> 273
ggggccgacc attatccaac cgggntcact gttgggtcat ctccctcctg 50
gatgaancc gccatcntca gactccctgc cccatggaga tttnnccat 100
gctggcgaca acatcntgac cccagccat gtacgagggg ctttgaacgt 150
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200
tgctgaatct gngcagcaca ttgcagcaac cntgccctg atggtgggtg 250
gcactcctct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300
tgtatgaagt gcttgaaga cgatgaggtg cagaagatga ggatggctgt 350
cattgggggc gcgatatttc ttcttgagc tctggctatt tnnngttgcc 400
acagcatggt atggcaatag aatcggtcaa gaattctatg accctatgac 450

cccagtcaat gccaggtagc aatttgggtca ggctctcttc actggctggg 500
 ctgctgcttc tctctgcctt ctgggaggtg ccctactttg ctgttcctgc 550
 ga 552

<210> 274
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407
 <223> unknown base

<400> 274
 attctcccct cctggatgga tgcgccacc gtcacattgc cttccccan 50
 tggaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100
 ttaccgaggg gctttggatg tontgcntgt cgcagagcac cgggcagatc 150
 ccagtgcaaa gtctttgact ccttgctgaa totgagcagc acattgcaag 200
 caaccctgctg cttgatgggg ttggcatcct cctgggagtg atagcaacct 250
 ttgtggccac cgttggcatg aagtgtatga agtgcttggg agacgatgag 300
 gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350
 caggtctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400
 cnngnnntct atgaccctat gacccagtc aatgccaggt acgaatttgg 450
 tcaggctctc ttactggct gggctgctgc ttctctctgc cttctgggag 500
 gtgccctact ttgctgttcc tgtccc 526

<210> 275
 <211> 398
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274
 <223> unknown base

<400> 275
 agagcaccgg cagatcccag tncaaagtct ttgacccttg ctgaatctga 50
 gcagcacatt ncaagcaacc ccttgccctg aaggtaggtg ncatcccccc 100
 tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150
 gtgcttggaa gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250
 tatggcaata gnatnnttcg nggntttctat gaccctatga cccagtcaa 300
 tgccagggtac gaatttggtc aggctctctt cactggctgg gctgctgctt 350
 ctctctgcct tctgggaggt gccctacttt gctgttcctg tccccgaa 398

<210> 276
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476
 <223> unknown base

<400> 276
 agcaatgccc tgccccagct ggaggattaa ttcctatgnt ggggacaaca 50
 ttgtgacngc ccaggccatg tacggggggc tgtggatgtc ctgctgtctg 100
 cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150
 gagcagcaca ttgcaagcaa cccgtgcctt gatggtggtt ggcattcttc 200
 tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250
 tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300
 cgcgatattt ctntttgcag gtctggctat tttagttgcc acagcatggt 350
 atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400
 gccagggtacg aatttggtca ggctttnttc actggctggg ctgctgcttn 450
 tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277
 <211> 200
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 34, 87, 138, 147, 163, 165-166, 172
 <223> unknown base

<400> 277
 tcataggggg gcgcgatatt ttttcttgca ggtntgggta ttttagttgc 50
 cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100
 cccagtcaa tgccagggtac gaatttggtc aggctctntt cactggntgg 150
 gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278
 <211> 542
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 26, 43, 55, 77, 198, 361-362, 391-392, 396
 <223> unknown base

<400> 278
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 ttacnccat gctggcgaac aacatcctga ccgcccaggc catgtacgag 100
 gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150
 aagtctttga ctcccttgctg aatctgagca gcacattgca agcaaccntg 200
 ccttgatggg ggttggcatc ctccctgggag tgatagcaat ctttgtggcc 250
 accgttggca tgaagtgta tgaagtgtt ggaagacgat gaggtgcaga 300
 agatgaggat ggtgtcatt gggggcgaga ttttcttct tgcaggctctg 350
 gctatcttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400
 tctatgaccc tatgaccca gtcaatgcca ggtacgaatt tggtcaggct 450
 ctcttcaactg gctgggctgc tgcttctctc tgccttctgg gaggtgcct 500
 actttgtgtg tctgtcccc gaaaaacaac ctcttaccga cg 542

<210> 279
 <211> 548
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 90, 115, 147, 228, 387
 <223> unknown base

<400> 279
 cggggctgca gctgttgggc ttcatctcgc ttccctgggat ggaatcggcg 50
 ccatcgtcag cactgccctg ccccatggag gatttactcn tatgctggcg 100
 acaacatcgt gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150
 tgctgcagag caccgggcag atccagtgc aagtctttga ctcccttgctg 200
 aatctgagca gcacattgca agcaaccntg ccttgatggg ggttggcatc 250
 ctccctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300
 gaagtgttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350

ggggcgcgat atttcttctt gcaggtctgg ctatttntag ttgccacagc 400
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450
tcaatgccag gtacgaatct ggctcaggtc tcttctactgg ctgggctgct 500
gcttctctct gccttctggg aggtgcccta ctttctgtgt cctgcgaa 548

<210> 280

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 280

cgagcgagtc atggccaacg c 21

<210> 281

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 281

gtgtcacacg tagtctttcc cgctgg 26

<210> 282

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 282

ctgcagctgt tgggcttcat tctgccttc ctgggatgga tcg 43

<210> 283

<211> 2285

<212> DNA

<213> Homo sapiens

<400> 283

gcgtgccgtc agctcgccgg gcaccgcggc ctgcacctcg cctccgccc 50

ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccacccgg 100

tagaggaccc ccgcccgtgc cccgaccggt ccccgccctt ttgtaaaact 150

taaagcgggc gcagcattaa cgcttcccgc cccggtgacc tctcaggggt 200

ctccccgcca aagggtgtcc gccgctaagg aacatggcga aggtggagca 250

ggtcctgagc ctgcagccgc agcacgagct caaattccga ggtcccttca 300

cccgatgttgt caccaccaac ctaaagcttg gcaaccogac agaccgaaat 350
 gtgtgttttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400
 caacagcgga atcatcgatg caggggcctc aattaatgta tctgtgatgt 450
 tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500
 gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550
 gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600
 ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650
 attatatcca caactgcac aaagacagaa acaccaatag tgtctaagtc 700
 tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750
 gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag 800
 ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850
 ccccatattca gcattagccc caactgggaa ggaagaaggc cttagcacc 900
 ggctcttggc tctggtggtt ttgttcttta tcgttggtgt aattattggg 950
 aagattgcct tgtagaggta gcatgcacag gatggtaa at tggattggtg 1000
 gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050
 aattaatgta tgatgacac tcacaggtct tgcctttaa ttaccctcc 1100
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 ttagaaagtt aaaaatgtat agtaactgat tgagggggaa aaagaatgat 1200
 ctttattaat gacaaggga accatgagta atgccacaat ggcatattgt 1250
 aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300
 tctcttaaaa tgacaccctt cctcgctgt tgggtgctggc ccttggggag 1350
 ctggagccca gcatgctggg gagtgcggtc agctccacac agtagtccc 1400
 acgtggccca ctcccgccc aggtgcttt ccgtgtcttc agttctgtcc 1450
 aagccatcag ctcttgga ctgatgaaca gagtcaag cccaaaggaa 1500
 ttgcaactgt gcagcatcag acgtactcgt cataagtga aggcgtgtgt 1550
 tgactgattg acccagcgt ttggaaata atggcagtgc tttgttact 1600
 taaagggacc aagctaaatt tgtattggt catgtagtga agtcaaactg 1650
 ttattcagag atgtttaatg catatttaac ttatttaatg tatttcatct 1700
 catgtttct tattgtcaca agagtacagt taatgctgcg tgctgctgaa 1750

ctctgttggg tgaactggta ttgctgctgg agggctgtgg gctcctctgt 1800
ctctggagag tctggatcatg tggaggtggg gtttattggg atgctggaga 1850
agagctgcca ggaagtgttt tttctgggtc agtaaataac aactgtcata 1900
gggagggaaa ttctcagtag tgacagtcaa ctctagggtta ctttttttaa 1950
tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000
actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050
ggacctagcc tggagtcagg acaaatggat cgggctgcag agggttagaa 2100
gcgagggcac cagcagttgt ggggtggggag caagggaaga gagaaactct 2150
tcagcgaatc cttctagtag tagttgagag tttgactgtg aattaatttt 2200
atgccataaa agaccaaccc agttctgttt gactatgtag catcttgaaa 2250
agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284
<211> 243
<212> PRT
<213> Homo sapiens

<400> 284
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1 5 10 15
Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu
20 25 30
Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys
35 40 45
Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile
50 55 60
Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro
65 70 75
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val
80 85 90
Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val
95 100 105
Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg
110 115 120
Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val
125 130 135
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr
140 145 150

Pro	Ile	Val	Ser	Lys	Ser	Leu	Ser	Ser	Ser	Leu	Asp	Asp	Thr	Glu
				155					160					165
Val	Lys	Lys	Val	Met	Glu	Glu	Cys	Lys	Arg	Leu	Gln	Gly	Glu	Val
				170					175					180
Gln	Arg	Leu	Arg	Glu	Glu	Asn	Lys	Gln	Phe	Lys	Glu	Glu	Asp	Gly
				185					190					195
Leu	Arg	Met	Arg	Lys	Thr	Val	Gln	Ser	Asn	Ser	Pro	Ile	Ser	Ala
				200					205					210
Leu	Ala	Pro	Thr	Gly	Lys	Glu	Glu	Gly	Leu	Ser	Thr	Arg	Leu	Leu
				215					220					225
Ala	Leu	Val	Val	Leu	Phe	Phe	Ile	Val	Gly	Val	Ile	Ile	Gly	Lys
				230					235					240

Ile Ala Leu

<210> 285
 <211> 418
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 40, 53, 68, 119, 134, 177-178, 255
 <223> unknown base

<400> 285
 gtcagtcttc tagattgtcc ttatcccacc tttcaaccan tactcacatt 50
 tcnagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100
 ctggagtcag gacaatggnt cgggctgcag aggnttagaa gcgagggcac 150
 cagcagtttt ggggtggggag caagggngga gagaaactct tcagcgaatc 200
 cttctagtag tagttgagag ttgactgtg aattaatttt atgccataaa 250
 agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
 taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
 ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
 gttaacttta aaatgagc 418

<210> 286
 <211> 543
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 73, 97

<223> unknown base

<400> 286

tattgtaaag	gccatttta	accattggta	ggccttggt	catgatgctg	50
gattacctcc	ttaaattgaca	ccnttcctcg	cctgttggtg	ctggccnttg	100
gggagctgga	gccccagcat	gctggggagt	gcggtcagct	ccacacagta	150
gtccccacgt	ggcccaactcc	cggcccaggc	tgctttccgt	gtcttcagtt	200
ctgtccaagc	catcagctcc	ttgggactga	tgaacagagt	cagaagccca	250
aaggaattgc	caactgtggca	gcacagacg	tactcgtcac	aagtgaagag	300
cggtgtgtga	ctgattgacc	cagcgctttg	gaaataaatg	gcagtgcctt	350
gttcaactta	agggaccaag	ctaaattgta	ttggttcacg	tagtgaagtc	400
aaactgttat	tcagagatgt	ttaatgcata	tttaacttat	ttaatgtatt	450
tcattctcatg	ttttcttatt	gtcacaagag	tacagttaat	gctgcgtgct	500
gctgaactct	gttggttgaa	ctggtattgc	tgctggaggg	ctg	543

<210> 287

<211> 270

<212> DNA

<213> Homo sapiens

 $\langle 220 \rangle$

<221> unsure

<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242

<223> unknown base

<400> 287

ccctgggtggt tttgttcttt aattcgttgg tgtaattntt gggaagattg 50
cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100
catatccatg ggatttaaatt ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcott taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaat gtatagtaac 270

<210> 288

<211> 428

<212> DNA

<213> Homo sapiens

 $\langle 220 \rangle$

<221> unsure

<222> 35, 116, 129, 197, 278, 294, 297, 349, 351

<223> unknown base

<400> 288
 ggtggcccat tcccggccca ggctgctttc cggtnnttcag ttctgtccaa 50
 gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100
 gcaactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150
 actgattgac ccagcgcttt ggaaataaat ggcagtgcctt tgttcantta 200
 aagggaccaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250
 attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300
 tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350
 ntgttgggtg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400
 ttggagagtc tggatcatgtg gaggtggg 428

<210> 289
 <211> 320
 <212> DNA
 <213> Homo sapiens

<400> 289
 tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50
 atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100
 tactogtcat aagtgaagagg cgtgtgttga ctgattgacc cagcgctttg 150
 gaaataaatg gcagtgcctt gtacacttaa agggaccaag ctaaatttgt 200
 attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250
 atttaactta tttaatgtat ttcactctcat gttttcttat tgtcacaaga 300
 gtacagttaa tgctgcgtgc 320

<210> 290
 <211> 609
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
 447, 481, 513, 532, 584, 598
 <223> unknown base

<400> 290
 aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50
 gaaacntgn gtaatgccac aatggcatat tgtaaattgc attttaaaca 100
 ttggtaggcc ttggtacatg atgctggatt acctctotta aaatgacacc 150
 cttcctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200

ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250
 cccaggctgc tttccgtgtc ttcagttctg tccaagccat cagctccttg 300
 ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350
 cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccagc 400
 gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450
 atttgatttg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500
 atgcatattt aanttattta atgtatttca tntcatgttt tcttattgtc 550
 acaaggttac agttaatgct gcgtgctgct gaantctgtt ggggtgaantg 600
 gtattgctg 609

<210> 291
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 291
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 cacagtagtc cccacgtggc ccaactcccgg cccaggctgc tttccgtgtc 100
 ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150
 aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
 gagaggcgtg tgttgactga ttgaccagc gctttggaaa taaatggcag 250
 tgctttgttc acttaaaggg accaagctaa atttgatttg gttcatgtag 300
 tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350
 atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400
 gcgtgctgct gaactctgtt ggggtgaactg gtattgctgc tggagggtg 450
 tgggctcctc tgtctctgga gactctggc atgtggaggt ggg 493

<210> 292
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 292
 gcaccaccgt aggtacttgt gtgaggc 27

<210> 293
 <211> 23
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccggctca 50

ggctggctga gaggctccca gctgcagcgt ccccgcccgc ctctcggga 100

gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150

gtctcacttt gttgccagg ctggagttca gtgccatgat catggtttac 200

tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250

acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300

atttttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350

attttatgtg gcacttgaga aaggtagccc ggattgtcag tgaaaggact 400

ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450

tacagtgtgt ggcacgaat gccagaaaga actcccaact cccagccttt 500

ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550

cgaaccttaa ccagggtgaa agttcaagat ttggtttcttg agccgactca 600

aaatatcacc acaaaggag tatctgttag gagaaagaga caggtgtatg 650

gcaccgacag caggttcagc atcttgga aaaggttctt aaccaatttc 700

cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcatttctcat 750

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 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450
 tgaggactat aggggtgaatt ctctgattag taattttaga tatgtccttt 2500
 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296

<211> 413

<212> PRT

<213> Homo sapiens

<400> 296

Met	Glu	Asn	Met	Leu	Leu	Trp	Leu	Ile	Phe	Phe	Thr	Pro	Gly	Trp	
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Thr	Leu	Ile	Asp	Gly	Ser	Glu	Met	Glu	Trp	Asp	Phe	Met	Trp	His	
				20					25					30	
Leu	Arg	Lys	Val	Pro	Arg	Ile	Val	Ser	Glu	Arg	Thr	Phe	His	Leu	
				35					40					45	
Thr	Ser	Pro	Ala	Phe	Glu	Ala	Asp	Ala	Lys	Met	Met	Val	Asn	Thr	
				50					55					60	
Val	Cys	Gly	Ile	Glu	Cys	Gln	Lys	Glu	Leu	Pro	Thr	Pro	Ser	Leu	
				65					70					75	
Ser	Glu	Leu	Glu	Asp	Tyr	Leu	Ser	Tyr	Glu	Thr	Val	Phe	Glu	Asn	
				80					85					90	
Gly	Thr	Arg	Thr	Leu	Thr	Arg	Val	Lys	Val	Gln	Asp	Leu	Val	Leu	
				95					100					105	
Glu	Pro	Thr	Gln	Asn	Ile	Thr	Thr	Lys	Gly	Val	Ser	Val	Arg	Arg	
				110					115					120	
Lys	Arg	Gln	Val	Tyr	Gly	Thr	Asp	Ser	Arg	Phe	Ser	Ile	Leu	Asp	
				125					130					135	
Lys	Arg	Phe	Leu	Thr	Asn	Phe	Pro	Phe	Ser	Thr	Ala	Val	Lys	Leu	
				140					145					150	
Ser	Thr	Gly	Cys	Ser	Gly	Ile	Leu	Ile	Ser	Pro	Gln	His	Val	Leu	
				155					160					165	
Thr	Ala	Ala	His	Cys	Val	His	Asp	Gly	Lys	Asp	Tyr	Val	Lys	Gly	
				170					175					180	
Ser	Lys	Lys	Leu	Arg	Val	Gly	Leu	Leu	Lys	Met	Arg	Asn	Lys	Ser	
				185					190					195	
Gly	Gly	Lys	Lys	Arg	Arg	Gly	Ser	Lys	Arg	Ser	Arg	Arg	Glu	Ala	
				200					205					210	

Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu
215 220 225

Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln
230 235 240

Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys
245 250 255

Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp
260 265 270

Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala
275 280 285

His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys
290 295 300

Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp
305 310 315

Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu
320 325 330

Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser
335 340 345

Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys
350 355 360

Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp
365 370 375

Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg
380 385 390

Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly
395 400 405

Asn Asp Ala Asn Cys Ala Tyr Gly
410

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcacctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 298
catcgttccc gtgaatccag aggc 24

<210> 299
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 299
gaagggaggc cttcctttca gtggacccgg gtcaagaata cccac 45

<210> 300
<211> 1869
<212> DNA
<213> Homo sapiens

<400> 300
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ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150
gcaactcctg gcacactgct cctctttctg gctttcctgc tcctgagttc 200
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250
gcccattggag tgaatgctca cgcacctgcg ggggaggggc ctcctactct 300
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350
cagaacatgc agtaatgtgg actgcccacc agaagcaggt gatttccgag 400
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gaatggcttc ctgtgtctaa tgaccctgac aaccatgtt cactcaagtg 500
ccaagccaaa ggaacaaccc tggttgttga actagcacct aaggtcttag 550
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cagaaatttc cagacaaaga gatactgaga atggctggac cactcacagc 950
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 taagtgtaat catctacca aagctttttg gctctcaa at taaagattga 1850
 ttagtttcaa aaaaaaaaa 1869

<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

Met	Glu	Cys	Cys	Arg	Arg	Ala	Thr	Pro	Gly	Thr	Leu	Leu	Leu	Phe
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Leu	Ala	Phe	Leu	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu
			20						25					30
Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys
			35						40					45
Ser	Arg	Thr	Cys	Gly	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys
			50						55					60

Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr	65	70	75
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala	80	85	90
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe	95	100	105
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser	110	115	120
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala	125	130	135
Pro	Lys	Val	Leu	Asp	Gly	Thr	Arg	Cys	Tyr	Thr	Glu	Ser	Leu	Asp	140	145	150
Met	Cys	Ile	Ser	Gly	Leu	Cys	Gln	Ile	Val	Gly	Cys	Asp	His	Gln	155	160	165
Leu	Gly	Ser	Thr	Val	Lys	Glu	Asp	Asn	Cys	Gly	Val	Cys	Asn	Gly	170	175	180
Asp	Gly	Ser	Thr	Cys	Arg	Leu	Val	Arg	Gly	Gln	Tyr	Lys	Ser	Gln	185	190	195
Leu	Ser	Ala	Thr	Lys	Ser	Asp	Asp	Thr	Val	Val	Ala	Leu	Pro	Tyr	200	205	210
Gly	Ser	Arg	His	Ile	Arg	Leu	Val	Leu	Lys	Gly	Pro	Asp	His	Leu	215	220	225
Tyr	Leu	Glu	Thr	Lys	Thr	Leu	Gln	Gly	Thr	Lys	Gly	Glu	Asn	Ser	230	235	240
Leu	Ser	Ser	Thr	Gly	Thr	Phe	Leu	Val	Asp	Asn	Ser	Ser	Val	Asp	245	250	255
Phe	Gln	Lys	Phe	Pro	Asp	Lys	Glu	Ile	Leu	Arg	Met	Ala	Gly	Pro	260	265	270
Leu	Thr	Ala	Asp	Phe	Ile	Val	Lys	Ile	Arg	Asn	Ser	Gly	Ser	Ala	275	280	285
Asp	Ser	Thr	Val	Gln	Phe	Ile	Phe	Tyr	Gln	Pro	Ile	Ile	His	Arg	290	295	300
Trp	Arg	Glu	Thr	Asp	Phe	Phe	Pro	Cys	Ser	Ala	Thr	Cys	Gly	Gly	305	310	315
Gly	Tyr	Gln	Leu	Thr	Ser	Ala	Glu	Cys	Tyr	Asp	Leu	Arg	Ser	Asn	320	325	330
Arg	Val	Val	Ala	Asp	Gln	Tyr	Cys	His	Tyr	Tyr	Pro	Glu	Asn	Ile	335	340	345
Lys	Pro	Lys	Pro	Lys	Leu	Gln	Glu	Cys	Asn	Leu	Asp	Pro	Cys	Pro			

350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His		
365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser		
380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu		
395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys		
410	415	420
Met Tyr Thr Pro Lys Met Pro Ile Ala Gln Pro Cys Asn Ile Phe		
425	430	435
Asp Cys Pro Lys Trp Leu Ala Gln Glu Trp Ser Pro Cys Thr Val		
440	445	450
Thr Cys Gly Gln Gly Leu Arg Tyr Arg Val Val Leu Cys Ile Asp		
455	460	465
His Arg Gly Met His Thr Gly Gly Cys Ser Pro Lys Thr Lys Pro		
470	475	480
His Ile Lys Glu Glu Cys Ile Val Pro Thr Pro Cys Tyr Lys Pro		
485	490	495
Lys Glu Lys Leu Pro Val Glu Ala Lys Leu Pro Trp Phe Lys Gln		
500	505	510
Ala Gln Glu Leu Glu Glu Gly Ala Ala Val Ser Glu Glu Pro Ser		
515	520	525

<210> 302
 <211> 1533
 <212> DNA
 <213> Homo sapiens

<400> 302
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 ctgggcgggg cgctgtggct ggcggcccg cggttcgtgg ggcccagggt 150
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 cgccgaggag gcggcggtc agctccgcc cgagctccgc caggccgcgg 350
 agtgcgggcc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400
 gagctggacc tcgcctcgct gcgctcggtg cgcgccttct gccaggaaat 450

gctccaggaa gagcctaggc tggatgtctt gatcaataac gcagggatct 500
tccagtgtccc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550
gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600
caaaagttca gctcccagca ggattgtggt agtttcttcc aaactttata 650
aatacggaga catcaatfff gatgacttga acagtgaaca aagctataat 700
aaaagctfff gttatagccg gagcaaaactg gctaacattc tttttaccag 750
ggaactagcc cgccgcttag aaggcacaaa tgtcaccgtc aatgtgttgc 800
atcctggtat tgtacggaca aatctgggga ggcacataca cattccactg 850
ttggtcaaac cactcttcaa tttggtgtca tgggctffff tcaaaaactcc 900
agtagaaggt gcccagactt ccatttattt ggcctcttca cctgaggtag 950
aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000
cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050
agtgatgggtt ggcctgctaa aataggaaca aggagtaaaa gagctgttta 1100
taaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150
acttgttact tgaagaaaaa gaatfffat attggaatag cctgctaaga 1200
ggtacatgtg ggtatfffgg agttactgaa aaattatfff tgggataaga 1250
gaatffcagc aaagatgtff taaatatata tagtaagtat aatgaataat 1300
aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350
tggatgacat attaatatff gtcagaatta agtgactcaa agtgctatcg 1400
agaggttfff caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
ttactacaat gtttggtggt tgtgtggaaa ttatctgcct ggtgtgtgca 1500
cacaagtctt acttggaata aatffactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly
1				5					10					15
Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln
				20					25					30
Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr
				35					40					45

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala		50	55	60
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg		65	70	75
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu		80	85	90
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly		95	100	105
Val	Gly	Glu	Leu	Ile	Val	Arg	Glu	Leu	Asp	Leu	Ala	Ser	Leu	Arg		110	115	120
Ser	Val	Arg	Ala	Phe	Cys	Gln	Glu	Met	Leu	Gln	Glu	Glu	Pro	Arg		125	130	135
Leu	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Phe	Gln	Cys	Pro	Tyr		140	145	150
Met	Lys	Thr	Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His		155	160	165
Leu	Gly	His	Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Gly	Leu	Leu	Lys		170	175	180
Ser	Ser	Ala	Pro	Ser	Arg	Ile	Val	Val	Val	Ser	Ser	Lys	Leu	Tyr		185	190	195
Lys	Tyr	Gly	Asp	Ile	Asn	Phe	Asp	Asp	Leu	Asn	Ser	Glu	Gln	Ser		200	205	210
Tyr	Asn	Lys	Ser	Phe	Cys	Tyr	Ser	Arg	Ser	Lys	Leu	Ala	Asn	Ile		215	220	225
Leu	Phe	Thr	Arg	Glu	Leu	Ala	Arg	Arg	Leu	Glu	Gly	Thr	Asn	Val		230	235	240
Thr	Val	Asn	Val	Leu	His	Pro	Gly	Ile	Val	Arg	Thr	Asn	Leu	Gly		245	250	255
Arg	His	Ile	His	Ile	Pro	Leu	Leu	Val	Lys	Pro	Leu	Phe	Asn	Leu		260	265	270
Val	Ser	Trp	Ala	Phe	Phe	Lys	Thr	Pro	Val	Glu	Gly	Ala	Gln	Thr		275	280	285
Ser	Ile	Tyr	Leu	Ala	Ser	Ser	Pro	Glu	Val	Glu	Gly	Val	Ser	Gly		290	295	300
Arg	Tyr	Phe	Gly	Asp	Cys	Lys	Glu	Glu	Glu	Leu	Leu	Pro	Lys	Ala		305	310	315
Met	Asp	Glu	Ser	Val	Ala	Arg	Lys	Leu	Trp	Asp	Ile	Ser	Glu	Val		320	325	330
Met	Val	Gly	Leu	Leu	Lys													

<210> 304
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 20, 34, 62, 87, 221, 229
 <223> unknown base

<400> 304
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 gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100
 ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150
 gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
 tttgatattg gaatagcctg ntaagaggna catgtgggta ttttggagtt 250
 actgaaaaat tatttttggg ataagagaat ttcagcaaag atgtttttaa 300
 tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
 attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
 gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
 tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500
 tggaattat ctgcctggct t 521

<210> 305
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 305
 ccaggaaatg ctccaggaag agcc 24

<210> 306
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 306
 gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307
aacgcagggg tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308
<211> 1523
<212> DNA
<213> Homo sapiens

<400> 308
gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50
cggagcccag ccttttcta acccaaccca acctagcca gtcccagccg 100
ccagcgcctg tccctgtcac ggaccccagc gttaccatgc atcctgccgt 150
cttcctatcc ttaccgagcc tcagatgctc ccttctgctc ctggtaactt 200
gggtttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250
atagatgaaa ttttaaacaa tgctgatgtt gctttagtaa atttttatgc 300
tgactgggtg cgtttcagtc agatgttgca tccaattttt gaggaagctt 350
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650
cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750
tggcgacaac ataatctaca aaccaccagg gcattctgct ccgatatgg 800
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850
gataaatgtg ttcctcttgt ccgagaaata acatttgaaa atggagagga 900
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000
agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050

acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100
ctattgacag ctttaggcac atgtatgtgt ttggagactt caaagatgta 1150
ttaattcctg gaaaactcaa gcaattogta tttgacttac attctggaaa 1200
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250
gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300
aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350
gctttaaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400
cctacgtggg ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450
tttatTTTga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309

<211> 406

<212> PRT

<213> Homo sapiens

<400> 309

Met	His	Pro	Ala	Val	Phe	Leu	Ser	Leu	Pro	Asp	Leu	Arg	Cys	Ser	1	5	10	15
Leu	Leu	Leu	Leu	Val	Thr	Trp	Val	Phe	Thr	Pro	Val	Thr	Thr	Glu	20	25	30	
Ile	Thr	Ser	Leu	Ala	Thr	Glu	Asn	Ile	Asp	Glu	Ile	Leu	Asn	Asn	35	40	45	
Ala	Asp	Val	Ala	Leu	Val	Asn	Phe	Tyr	Ala	Asp	Trp	Cys	Arg	Phe	50	55	60	
Ser	Gln	Met	Leu	His	Pro	Ile	Phe	Glu	Glu	Ala	Ser	Asp	Val	Ile	65	70	75	
Lys	Glu	Glu	Phe	Pro	Asn	Glu	Asn	Gln	Val	Val	Phe	Ala	Arg	Val	80	85	90	
Asp	Cys	Asp	Gln	His	Ser	Asp	Ile	Ala	Gln	Arg	Tyr	Arg	Ile	Ser	95	100	105	
Lys	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Arg	Asn	Gly	Met	Met	Met	Lys	110	115	120	
Arg	Glu	Tyr	Arg	Gly	Gln	Arg	Ser	Val	Lys	Ala	Leu	Ala	Asp	Tyr	125	130	135	
Ile	Arg	Gln	Gln	Lys	Ser	Asp	Pro	Ile	Gln	Glu	Ile	Arg	Asp	Leu	140	145	150	
Ala	Glu	Ile	Thr	Thr	Leu	Asp	Arg	Ser	Lys	Arg	Asn	Ile	Ile	Gly	155	160	165	

Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg
				170					175					180
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe
				185					190					195
Gly	Asp	Val	Ser	Lys	Pro	Glu	Arg	Tyr	Ser	Gly	Asp	Asn	Ile	Ile
				200					205					210
Tyr	Lys	Pro	Pro	Gly	His	Ser	Ala	Pro	Asp	Met	Val	Tyr	Leu	Gly
				215					220					225
Ala	Met	Thr	Asn	Phe	Asp	Val	Thr	Tyr	Asn	Trp	Ile	Gln	Asp	Lys
				230					235					240
Cys	Val	Pro	Leu	Val	Arg	Glu	Ile	Thr	Phe	Glu	Asn	Gly	Glu	Glu
				245					250					255
Leu	Thr	Glu	Glu	Gly	Leu	Pro	Phe	Leu	Ile	Leu	Phe	His	Met	Lys
				260					265					270
Glu	Asp	Thr	Glu	Ser	Leu	Glu	Ile	Phe	Gln	Asn	Glu	Val	Ala	Arg
				275					280					285
Gln	Leu	Ile	Ser	Glu	Lys	Gly	Thr	Ile	Asn	Phe	Leu	His	Ala	Asp
				290					295					300
Cys	Asp	Lys	Phe	Arg	His	Pro	Leu	Leu	His	Ile	Gln	Lys	Thr	Pro
				305					310					315
Ala	Asp	Cys	Pro	Val	Ile	Ala	Ile	Asp	Ser	Phe	Arg	His	Met	Tyr
				320					325					330
Val	Phe	Gly	Asp	Phe	Lys	Asp	Val	Leu	Ile	Pro	Gly	Lys	Leu	Lys
				335					340					345
Gln	Phe	Val	Phe	Asp	Leu	His	Ser	Gly	Lys	Leu	His	Arg	Glu	Phe
				350					355					360
His	His	Gly	Pro	Asp	Pro	Thr	Asp	Thr	Ala	Pro	Gly	Glu	Gln	Ala
				365					370					375
Gln	Asp	Val	Ala	Ser	Ser	Pro	Pro	Glu	Ser	Ser	Phe	Gln	Lys	Leu
				380					385					390
Ala	Pro	Ser	Glu	Tyr	Arg	Tyr	Thr	Leu	Leu	Arg	Asp	Arg	Asp	Glu
				395					400					405

Leu

<210> 310
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure

<222> 36, 48
<223> unknown base

<400> 310
attaaggaag aatttccaaa tgaaaatcaa gtagtntttg ccagagtnga 50
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396
<223> unknown base

<400> 311
agaggcctct ctggaagttg tcccggtgt tcgccgngg agcccgggtc 50
gagaggacna ggtgccgtg cctggagaat cctccgctgc cgtcggctcc 100
cggagcccag ccctttccta acccaaccca acctagccn gtcccagccg 150
ccagcgctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200
cttcctatcc ttaccgcgacc tcagatgctc ccttctgctc ctggtaactt 250
gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300
atagatgaaa ttttaaacna tgctgatgtg gcttttagtca atttttatgc 350
tgactggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 312
tgagaggcct ctctggaagt tg 22

<210> 313
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 313
 gtcagcgatc agtgaaagc 19

<210> 314
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 314
 ccagaatgaa gtagctcggc 20

<210> 315
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 315
 ccgactcaaa atgcattgtc 20

<210> 316
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 316
 catttggcag gaattgtcc 19

<210> 317
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 317
 ggtgctatag gccaaggg 18

<210> 318
 <211> 24
 <212> DNA

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	50.5 (10.5)
Female	51.5 (11.5)
Marital status	
Married	75.5%
Single	24.5%
Education level	
High school or above	65.5%
Below high school	34.5%
Occupation	
Professional	15.5%
Managerial	10.5%
Technical	15.5%
Service	25.5%
Skilled	15.5%
Unskilled	17.5%
Retired	5.5%
Income (US\$)	
<1000	15.5%
1000-2000	25.5%
2000-3000	15.5%
>3000	43.5%
Health insurance	
Yes	85.5%
No	14.5%
Smoking status	
Smoker	15.5%
Non-smoker	84.5%
Alcohol consumption	
Yes	15.5%
No	84.5%
Comorbidities	
Hypertension	35.5%
Diabetes	15.5%
Cholesterol	25.5%
Obesity	15.5%
Family history of cancer	
Yes	15.5%
No	84.5%

tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaaatt gtttccacat 600
 ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650
 taaatggtat tacgtataaa ttaatatataa atgattacct ctggtgttga 700
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800
 cttgtagggc tcatttttgt ttcatgaaa cagtatctaa ttataaatta 850
 gctgtagata tcagggtgctt ctgatgaagt gaaaatgtat atctgactag 900
 tgggaaactt catgggttcc ctcatctgtc atgtcgatga ttatatatgg 950
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050
 taaatatact tgctttaatt cttaagcata agtaaacadg atataaaaaat 1100
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaatgtgt 1150
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200
 ttctaactctg gtggtaaagg tattcttaag aatttgcagg tactacagat 1250
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 322
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu
 1 5 10 15
 Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala
 20 25 30
 Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys
 35 40 45
 Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala
 50 55 60
 Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu
 65 70 75
 Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met
 80 85 90
 Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr
 95 100 105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp
 110 115 120
 Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr
 125 130 135
 Gly Met Ile Tyr Val Leu Val Ser Ser
 140

<210> 323
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 323
 attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50
 tgtaataccc tgaatcccct tgtactccca gagtacctca tccacgcttt 100
 cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150
 atatgcccct cttggcatat catatttgga ggtatatgag tagaccagtg 200
 atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250
 tctagcatat tgtcagaagg aaggatggtg caaattagct ttttatcttc 300
 tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350
 tagaacaaca cacagaagaa ttggtccagt taagtgcagc caaaaagcca 400
 ccaaataaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450
 gaatctgata agttacttta aaaaatg 477

<210> 324
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 324
 tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 325
 caggaaacag ctatgaccac ctgcacacct gcaaataccat t 41

<210> 326

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaccaa ttcttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tgggtgcaaat tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50
tgtgacagag gggaacaaga tggcggcgcc gaagggggagc ctctgggtga 100
ggacccaact ggggctcccg ccgctgctgc tgctgaccat ggccttggcc 150
ggaggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250
accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300
tcaatttgtc agtttgtgga tgatggaatt gacttaaadc gaactaaatt 350
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450
caagaacaac ttatgtccct gatgcaaaa atgcacctac tctttcctct 500

Leu	Pro	Phe	Ala	Glu	Leu	Arg	Gln	Glu	Gln	Leu	Met	Ser	Leu	Met	
				125					130					135	
Pro	Lys	Met	His	Leu	Leu	Phe	Pro	Leu	Thr	Leu	Val	Arg	Ser	Phe	
				140					145					150	
Trp	Ser	Asp	Met	Met	Asp	Ser	Ala	Gln	Ser	Phe	Ile	Thr	Ser	Ser	
				155					160					165	
Trp	Thr	Phe	Tyr	Leu	Gln	Ala	Asp	Asp	Gly	Lys	Ile	Val	Ile	Phe	
				170					175					180	
Gln	Ser	Lys	Pro	Glu	Ile	Gln	Tyr	Ala	Pro	His	Leu	Glu	Gln	Glu	
				185					190					195	
Pro	Thr	Asn	Leu	Arg	Glu	Ser	Ser	Leu	Ser	Lys	Met	Ser	Tyr	Leu	
				200					205					210	
Gln	Met	Arg	Asn	Ser	Gln	Ala	His	Arg	Asn	Phe	Leu	Glu	Asp	Gly	
				215					220					225	
Glu	Ser	Asp	Gly	Phe	Leu	Arg	Cys	Leu	Ser	Leu	Asn	Ser	Gly	Trp	
				230					235					240	
Ile	Leu	Thr	Thr	Thr	Leu	Val	Leu	Ser	Val	Met	Val	Leu	Leu	Trp	
				245					250					255	
Ile	Cys	Cys	Ala	Thr	Val	Ala	Thr	Ala	Val	Glu	Gln	Tyr	Val	Pro	
				260					265					270	
Ser	Glu	Lys	Leu	Ser	Ile	Tyr	Gly	Asp	Leu	Glu	Phe	Met	Asn	Glu	
				275					280					285	
Gln	Lys	Leu	Asn	Arg	Tyr	Pro	Ala	Ser	Ser	Leu	Val	Val	Val	Arg	
				290					295					300	
Ser	Lys	Thr	Glu	Asp	His	Glu	Glu	Ala	Gly	Pro	Leu	Pro	Thr	Lys	
				305					310					315	
Val	Asn	Leu	Ala	His	Ser	Glu	Ile								
				320											

<210> 331
 <211> 350
 <212> DNA
 <213> Homo sapiens

<400> 331
 ttgggtgata cggcgtcttg ccaccgggccc tgtcagttga cctaccctt 50
 gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 100
 ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaactga 150
 actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200
 tgagcaatat gcttgccatc ttgggttgcca gaatcagctg ccattcgctg 250

aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300
 ttctctctaa ctctgggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332
 <211> 562
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 47
 <223> unknown base

<400> 332
 cacactggcc ggatctttta gagtcctttg accttgacca agggctcngga 50
 aaacagcaac aagctgagct gctgtgacag agggaacaag atggcggcgc 100
 cgaagggagc ctttgggtga ggacccaact ggggctcccg ccgctgctgc 150
 tgctgaccat ggccttggcc ggaggttcgg ggaccgcttc ggctgaagca 200
 ttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250
 gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300
 agagaggttg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350
 gacttaaadc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400
 ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450
 tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500
 atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550
 gatggactcc gc 562

<210> 333
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 333
 acaagctgag ctgctgtgac ag 22

<210> 334
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 334
tgattctggc aaccaagatg gc 22

<210> 335
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 335
atggccttgg ccggaggttc ggggaccgct tcggctgaag 40

<210> 336
<211> 1885
<212> DNA
<213> Homo sapiens

<400> 336
gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50
cggcccggag gtggggcgcc gctggggccg gcccgcacgg gcttcatctg 100
agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150
gcgacaagct gccggagctg caatgggccc cggtctgggga ttcttgtttg 200
gcctcctggg cgccgtgttg ctgctcagct cgggccacgg agaggagcag 250
cccccggaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300
ggatgattgt acctgtgatg ttgaaacct tgatagattt aataactaca 350
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600
tctgagtgaag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800
agccacagac aattaaaaga cttttaaatc ctttggttc tggtaaggg 850
acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900
aaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950

tgcatttgag tgcaagatat cttttacaag agacctgggt agaaaagaaa 1000
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatgtt ctctacttaa 1100
 tagaactaag ggctttatcc aaagtgttac cattcttcga ggcgccagat 1150
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatgtt 1200
 acttctggaa atacttcacg aaatcaagtc atttcctttg ctttttgatg 1250
 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300
 gactttcgac tgcattttag aaatatattca agaattatgg attgtgttgg 1350
 ttgtttttaa tgtcgtctgt ggggaaagct tcagactcag ggtttgggca 1400
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450
 agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500
 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650
 atagcaatga cagtcttaag ccaaacattt tatataaagt tgctttttgta 1700
 aaggagaatt atattgtttt aagtaaacac atttttataa attgtgttaa 1750
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgttgt 1800
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattataa 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337
 <211> 468
 <212> PRT
 <213> Homo sapiens

<400> 337
 Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val
 1 5 10 15
 Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr
 20 25 30
 Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp
 35 40 45
 Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg
 50 55 60
 Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg
 65 70 75

Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp	80	85	90
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln	95	100	105
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr	110	115	120
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu	125	130	135
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys	140	145	150
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe	155	160	165
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp	170	175	180
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp	185	190	195
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys	200	205	210
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln	215	220	225
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu	230	235	240
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His	245	250	255
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu	260	265	270
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln	275	280	285
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg	290	295	300
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu	305	310	315
Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	320	325	330
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	335	340	345
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	350	355	360
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys			

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 339
 aagctgccgg agctgcaatg 20

 <210> 340
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 340
 ttgcttctta atcctgagcg c 21

 <210> 341
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 341
 aaaggaggac tttcgactgc 20

 <210> 342
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 342
 agagattcat ccactgctcc aagtcg 26

 <210> 343
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 343
 tgtccagaaa caggcacata tcagc 25

 <210> 344
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tgggcggacg cgtgggttgg gagggggcag 50
gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100
ggactttctca tactggacag aaaccgatca ggcattggaac tccccttcgt 150
cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200
ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250
gaatttggat acagtgtctt acaacatgtt ggggggtggac agcgatggat 300
gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350
tttatcgctg ccctgtaggg ggggcccaca atgccccatg tgccaagggc 400
cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450
gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500
tgagctaagg agaggggtgg ggcagtgtct ctgaagggtcc ataaaagaaa 550
aaagagaagt gtggtgaagg aaaatggtct gtgtggaggg gtcaaggagt 600
taaaaaccct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650
gctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700
gtaactattt ccccatccc caggcctgtg cccctctctg gtctcgtgct 750
tgtggcagct ctgtcttcag ttctgggata tgtgccctg tggatgcttc 800
attccagcct cagggaagcc tggcaccac tgcccaacgt gagccagagg 850
aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900
gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc tatcctcatt 950
gctacctaata gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000
cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050
caagggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100
catggtgaaa ctccatctct actaaaaaaa aaaaaatata aaaattagct 1150

gggtgcgcta gtgcatgcct gtaatctcat ctactcgga ggctaagaca 1200
 ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250
 gtgcctctgc actctagcgt gggtagacaga gtaagcgaga ctccatctca 1300
 aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350
 gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
 gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450
 agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 346
 Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe
 1 5 10 15
 Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro
 20 25 30
 Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val
 35 40 45
 Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala
 50 55 60
 Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg
 65 70 75
 Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His
 80 85 90
 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn
 95 100 105
 Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly
 110 115 120
 Phe Met Val Ser

<210> 347
 <211> 509
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 22
 <223> unknown base

<400> 347

cacagttccc caccatcact cntcccatc cttccaactt tatttttagc 50
 ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
 ggagagggac agaggccaga ggacttctca tactggacag aaaccgatca 150
 ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttct 200
 gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250
 tcccagggcc accagaagct gaatttggat acagtgtctt acaacatgtt 300
 gggggtggac agcgatggat gctggtgggc gccccctggg atgggccttc 350
 aggcgaccgg aggggggacg tttatcgctg ccctgtaggg gggggccaca 400
 atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
 tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500
 tggatgatgg 509

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 348
 agggacagag gccagaggac ttc 23

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 349
 caggtgcata ttcacagcag gatg 24

<210> 350
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 350
 ggaactcccc ttcgtcactc acctgttctt gcccttggtg ttcct 45

<210> 351
 <211> 2056
 <212> DNA

<213> Homo sapiens

<400> 351

aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50
catctggggt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100
gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200
gctttatfff ggaaagaaac aatgttctag gtcaaactga gtctacaaaa 250
tgcagacttt cacaatgggt ctagaagaaa totggacaag tcttttcatg 300
tggtttttct acgcattgat tccatgtttg ctacacagatg aagtggccat 350
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400
tcttgatgtg gagcccagtg atcgcgccctg gagaaacagt gtactattct 450
gtcgaatacc agggggagta cgagagccctg tacacgagcc acatctggat 500
ccccagcagc tgggtgctcac tcaactgaagg tcttgagtgt gatgtcactg 550
atgacatcac ggccactgtg ccatacaacc ttctgtgtcag ggccacattg 600
ggctcacaga cctcagcctg gagcatcctg aagcatcoot ttaatagaaa 650
ctcaaccatc cttacccgac ctgggatgga gatcaccaaa gatggcttcc 700
acctggttat tgagctggag gacctggggc ccagtttga gttccttgtg 750
gcctactgga ggaggagcc tggtgccgag gaacatgtca aaatgggtgag 800
gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850
actgtgtgaa ggcccagaca ttctgtgaagg ccattgggag gtacagcgcc 900
ttcagccaga cagaatgtgt ggagggtgcaa ggagaggcca ttcccctggt 950
actggccctg tttgcctttg ttggcttcat gctgacctt gtggctcgtgc 1000
cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050
gtggtggtcc tcccagacac cttgaaaata accaattcac cccagaagtt 1100
aatcagctgc agaaggagg aggtggatgc ctgtgccacg gctgtgatgt 1150
ctcctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200
cagggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250
aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300
gagcctgttg totacaagtc tagaagcaac catcagaggc agggtggttt 1350
gtctaacaga aactgactg aggccttaggg gatgtgacct ctagactggg 1400

ggctgccact tgctggctga gcaaccctgg gaaaagtgc ttcattccctt 1450
 cggctcctaag ttttctcatc tgtaatgggg gaattaccta cacacctgct 1500
 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550
 tacacccagc acttgcaagg cttagaggaa actgggtgaca ctctacagtc 1600
 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650
 gatcaaggac tctacacact ggggtggcttg gagagcccac tttcccagaa 1700
 taatccttga gagaaaagga atcatgggag caatgggtgt gagttcactt 1750
 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800
 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950
 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050
 aaaaaa 2056

<210> 352

<211> 311

<212> PRT

<213> Homo sapiens

<400> 352

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu
1				5				10						15
Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
			20					25						30
Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser
			35					40						45
Thr	Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro
			50					55						60
Gly	Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu
			65					70						75
Ser	Leu	Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser
			80					85						90
Leu	Thr	Glu	Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala
			95					100						105
Thr	Val	Pro	Tyr	Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln
			110					115						120

Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser
				125					130					135
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe
				140					145					150
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe
				155					160					165
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val
				170					175					180
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met
				185					190					195
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys
				200					205					210
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu
				215					220					225
Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe
				230					235					240
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp
				245					250					255
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val
				260					265					270
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile
				275					280					285
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met
				290					295					300
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser				
				305					310					

<210> 353
 <211> 864
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 654, 711, 748, 827
 <223> unknown base

<400> 353
 tcctgctgat gcacatctgg gtttggcaaa aggaggttgc ttcgagccgc 50
 cttttctagc ttctggccg gctctagaac aattcaggct tcgctgcgac 100
 tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150
 agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200

ccaaatgcag actttcaciaa tggttctaga agaaatctgg acaagtcttt 250
 tcatgtgggt tttctacgca ttgattccat gtttgctcac agatgaagtg 300
 gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400
 attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450
 tggatcccca gcagctgggt ctcaactcact gaaggctctg agtgtgatgt 500
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
 cattgggctc acagacctca gcctggagca tctgaagca tccctttaat 600
 agaaactcaa ccatccttac ccgacctggg atggagatca ccaaagatgg 650
 cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700
 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
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 <220>
 <223> Synthetic oligonucleotide probe

 <400> 354
 aggcttcgct gcgactagac ctc 23

 <210> 355
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 <220>
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 <400> 355
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Ser Tyr Lys Asn Asp Ala Tyr Phe Leu	Gln Asp Leu Ser Leu Glu	
215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe	Ile Thr Tyr Gln Gly Ser	
230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr	Val Thr Trp Ile Leu Ile	
245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu	Gln Met His Ser Leu Arg	
260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln	Ile Phe Gln Ser Leu Ser	
275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu	Ala His Arg Ala Leu Arg	
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<211> 3038

<212> DNA

<213> Homo sapiens

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<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

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				20					25					30
Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu
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Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn
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Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln
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Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val
				80					85					90
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp
				95					100					105
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu
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Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln
				125					130					135
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His
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Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys
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Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly

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Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly					
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Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser					
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Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys					
				230					235					240					
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu					
				245					250					255					
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His					
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Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser					
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Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg					
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Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala					
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Gly	Cys	Leu	Asp	Ser	Lys	Ala	Lys	Val	Ile	Gly	Ser	Val	His	Tyr					
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Glu	Met	Gln	Ser	Ser	Ile	Cys	Arg	Ala	Ala	Ile	His	Tyr	Gly	Ile					
				335					340					345					
Ile	Asp	Asn	Asp	Gly	Gly	Trp	Val	Asp	Ile	Thr	Arg	Gln	Gly	Arg					
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Lys	His	Tyr	Phe	Ile	Lys	Ser	Asn	Arg	Asn	Gly	Ile	Gln	Thr	Ile					
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Gly	Lys	Tyr	Gln	Ser	Ala	Asn	Ser	Phe	Thr	Val	Ser	Lys	Val	Thr					
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Val	Gln	Ala	Val	Thr	Cys	Glu	Thr	Thr	Val	Glu	Gln	Leu	Cys	Pro					
				395					400					405					
Phe	His	Lys	Pro	Ala	Ser	His	Cys	Pro	Arg	Val	Tyr	Cys	Pro	Arg					
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Asn	Cys	Met	Gln	Ala	Asn	Pro	His	Tyr	Ala	Arg	Val	Ile	Gly	Thr					
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Arg	Val	Tyr	Ser	Asp	Leu	Ser	Ser	Ile	Cys	Arg	Ala	Ala	Val	His					
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Ala	Gly	Val	Val	Arg	Asn	His	Gly	Gly	Tyr	Val	Asp	Val	Met	Pro					
				455					460					465					

Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile
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Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg
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Val Phe Ala Val Val
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<210> 366
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aaccactcca gcatgtactg ctgc 24

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 <213> Homo sapiens

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 Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys
 35 40 45
 Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
 50 55 60
 Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val
 65 70 75
 Ser Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln
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 Arg Arg Val Tyr Glu Glu
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<223> Synthetic oligonucleotide probe

<400> 371

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<210> 372

<211> 24

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<212> DNA

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<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

Met	Leu	Asn	Ser	Asn	Val	Leu	Leu	Trp	Leu	Thr	Ala	Leu	Ala	Ile
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Lys	Phe	Thr	Leu	Ile	Asp	Ser	Gln	Ala	Gln	Tyr	Pro	Val	Val	Asn
			20					25						30

Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
			35					40						45

Glu Ile Leu Gly Pro Val Glu Gln Tyr Leu Gly Val Pro Tyr Ala

50										55					60				
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro					
				65					70					75					
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val					
				80					85					90					
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu					
				95					100					105					
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val					
				110					115					120					
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro					
				125					130					135					
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr					
				140					145					150					
Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser					
				155					160					165					
Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Glu					
				170					175					180					
Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly					
				185					190					195					
Asn	Val	Ile	Val	Ile	Thr	Ile	Asn	Tyr	Arg	Leu	Gly	Ile	Leu	Gly					
				200					205					210					
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu					
				215					220					225					
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Glu	Glu	Asn	Val	Gly					
				230					235					240					
Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly					
				245					250					255					
Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser					
				260					265					270					
Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu					
				275					280					285					
Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile					
				290					295					300					
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met					
				305					310					315					
Val	Glu	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Glu	Leu	Ile	Gln	Gln					
				320					325					330					
Thr	Ile	Thr	Pro	Ala	Thr	Tyr	His	Ile	Ala	Phe	Gly	Pro	Val	Ile					
				335					340					345					

Asp Gly Asp Val	Ile Pro Asp Asp Pro	Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu	Asn Tyr Asp Ile Met	Leu Gly Val Asn Gln Gly	365	370	375
Glu Gly Leu Lys	Phe Val Asp Gly Ile	Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn	Asp Phe Asp Phe Ser	Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly	Tyr Pro Glu Gly Lys	Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met	Tyr Thr Asp Trp Ala	Asp Lys Glu Asn Pro Glu	425	430	435
Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn			

635	640	645
Asn Pro Lys His Ser Lys Asp Pro His	Lys Thr Gly Pro Glu Asp	
650	655	660
Thr Thr Val Leu Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu Leu	
665	670	675
Ser Val Thr Ile Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn Ile	
680	685	690
Leu Ala Phe Ala Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg His	
695	700	705
Glu Thr His Arg Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn Asp	
710	715	720
Ile Ala His Ile Gln Asn Glu Glu Ile	Met Ser Leu Gln Met Lys	
725	730	735
Gln Leu Glu His Asp His Glu Cys Glu	Ser Leu Gln Ala His Asp	
740	745	750
Thr Leu Arg Leu Thr Cys Pro Pro Asp	Tyr Thr Leu Thr Leu Arg	
755	760	765
Arg Ser Pro Asp Asp Ile Pro Leu Met	Thr Pro Asn Thr Ile Thr	
770	775	780
Met Ile Pro Asn Thr Leu Thr Gly Met	Gln Pro Leu His Thr Phe	
785	790	795
Asn Thr Phe Ser Gly Gly Gln Asn Ser	Thr Asn Leu Pro His Gly	
800	805	810
His Ser Thr Thr Arg Val		
815		

<210> 376
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 376
 ggcaagctac ggaaacgtca tcgtg 25

<210> 377
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

gggaaagatg gcggcgactc tgggacccct tgggtcgtgg cagcagtggc 50

ggcgatgttt gtcggctcgg gatgggtcca ggatgttact ccttcttctt 100

ttgttgggggt ctgggcaggg gccacagcaa gtcggggcgg gtcaaacgtt 150

cgagtacttg aaacgggagc actcgctgtc gaagccctac cagggtgtgg 200

gcacaggcag ttctcactg tggaaatctga tgggcaatgc catggtgatg 250

accaggtata tccgccttac ccagatatg caaagtaaac aggggtgcctt 300

gtggaaccgg gtgccatgtt tctgagaga ctgggagttg cagggtgcact 350

tcaaaatcca tggacaagga aagaagaatc tgcattgggga tggcttggca 400

atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaacat 450

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gctgcctgag atgacagctc cactgcggcc cctgagtggc ctggccctct 950

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 gccgcgactc tagagtgcac ctgcagtagg gataacagg taataagctt 2450

Ile Thr Gly Asp	Leu Ser Asp Asn His	Asp Val Ile Ser Leu Lys
260	265	270
Leu Phe Glu Leu	Thr Val Glu Arg Thr	Pro Glu Glu Glu Lys Leu
275	280	285
His Arg Asp Val	Phe Leu Pro Ser Val	Asp Asn Met Lys Leu Pro
290	295	300
Glu Met Thr Ala	Pro Leu Pro Pro Leu	Ser Gly Leu Ala Leu Phe
305	310	315
Leu Ile Val Phe	Phe Ser Leu Val Phe	Ser Val Phe Ala Ile Val
320	325	330
Ile Gly Ile Ile	Leu Tyr Asn Lys Trp	Gln Glu Gln Ser Arg Lys
335	340	345

Arg Phe Tyr

<210> 381
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 381
 ccttgggtcg tggcagcagt gg 22

<210> 382
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 382
 cactctccag gctgcatgct cagg 24

<210> 383
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 383
 gtcaaacgtt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384
 <211> 3150
 <212> DNA
 <213> Homo sapiens

<400> 384

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 ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150
 tggggctctgg ctcaagaattc ctgcagctgg tgaaaatctg ttttctagaa 200
 gaggtttaat taatgcctgc agtctgacat gttcccgatt tgaggtgaaa 250
 ccatgaagag aaaatagaat acttaataat gcttttccgc aaccgcttct 300
 tgctgctgct ggccctggct gcgctgctgg cctttgtgag cctcagcctg 350
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 actggattca tttttaaac attttcatca gtttcaaattg gtaaattctg 2900

Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe	215	220	225
Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe	230	235	240
Cys	Ser	Gly	Ser	Cys	Tyr	Cys	Pro	Val	Arg	Asn	Gln	Tyr	Leu	Glu	245	250	255
Lys	Glu	Gln	Arg	Arg	Gln	Tyr	Leu	Leu	Arg	Leu	Lys	Asn	Ser	Gln	260	265	270
Leu	Glu	Lys	Thr	Tyr	Gly	Glu	Met	Ala	Lys	Ile	Val	Asp	Val	Pro	275	280	285
Thr	Lys	Gln	Leu	Arg	Ala	Ala	Asn	Pro	Ile	Asp	Ser	Met	Leu	Cys	290	295	300
His	Phe	Cys	His	Asn	Val	Ser	Phe	Pro	Cys	Thr	Arg	Asn	Gly	Cys	305	310	315
Val	Asp	Met	Glu	His	Phe	Lys	Val	Ile	Lys	Thr	His	Gln	Ile	Glu	320	325	330
Asp	Glu	Arg	Glu	Arg	Arg	Glu	Lys	Lys	Leu	Tyr	Phe	Gly	Tyr	Ser	335	340	345
Leu	Leu	Gly	Ala	His	Pro	Ile	Leu	Asn	Gln	Thr	Ile	Gly	Arg	Met	350	355	360
Gln	Arg	Ala	Thr	Glu	Gly	Arg	Lys	Glu	Glu	Leu	Phe	Ala	Leu	Tyr	365	370	375
Ser	Ala	His	Asp	Val	Thr	Leu	Ser	Pro	Val	Leu	Ser	Ala	Leu	Gly	380	385	390
Leu	Ser	Glu	Ala	Arg	Phe	Pro	Arg	Phe	Ala	Ala	Arg	Leu	Ile	Phe	395	400	405
Glu	Leu	Trp	Gln	Asp	Arg	Glu	Lys	Pro	Ser	Glu	His	Ser	Val	Arg	410	415	420
Ile	Leu	Tyr	Asn	Gly	Val	Asp	Val	Thr	Phe	His	Thr	Ser	Phe	Cys	425	430	435
Gln	Asp	His	His	Lys	Arg	Ser	Pro	Lys	Pro	Met	Cys	Pro	Leu	Glu	440	445	450
Asn	Leu	Val	Arg	Phe	Val	Lys	Arg	Asp	Met	Phe	Val	Ala	Leu	Gly	455	460	465
Gly	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Ala	Cys	His	Arg	Glu	Gly	Phe	470	475	480

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 386
ccaagcagct tagagctcca gacc 24

<210> 387
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 387
ttccctatgc tctgtattgg catgg 25

<210> 388
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 388
gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389
<211> 3313
<212> DNA
<213> Homo sapiens

<400> 389
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cccttttgaa gaacagtact gtggagctat ttaagagata aaaacgaaat 100
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gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200
cacgcgcctg aagcacaaaag cagatagcta ggaatgaacc atccctggga 250
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cgaccccgac tgtgaagaga acgccagat cacttattcc ctggctgaga 1850
acaccatcca aggggcaagc ctatcgtcct acgtgtccat caactccgac 1900
actggggtac tgtatgcgct gagctccttc gactacgagc agttccgaga 1950
cttgcaagtg aaagtgatgg cgcgggacaa cgggcacccg cccctcagca 2000
gcaacgtgtc gttgagcctg ttcgtgctgg accagaacga caatgcgccc 2050

gagatcctgt accccgccct ccccaaggac ggttccactg gcgtggagct 2100
 ggctccccgc tccgcagagc ccggtacct ggtgaccaag gtggtggcgg 2150
 tggacagaga ctccggccag aacgcctggc tgtcctaccg tctgctcaag 2200
 gccagcgagc cgggactctt ctcggtgggt ctgcacacgg gcgaggtgcg 2250
 cacggcgcgga gccctgctgg acagagacgc gctcaagcag agcctcgtag 2300
 tggccgtcca ggaccacggc cagccccctc tctccgccac tgtcacgctc 2350
 accgtggccg tggccgacag catcccccaa gtcttgccgg acctcggcag 2400
 cctcgagtct ccagctaact ctgaaacctc agacctcact ctgtacctgg 2450
 tggtagcggg ggccgcgggc tcttgctctt tcttgccctt cgtcatcttg 2500
 ctgctggcgc tcaggctgcg gcgctggcac aagtcacgcc tgctgcaggc 2550
 ttcaggaggc ggcttgacag gagcgccggc gtcgcacttt gtgggcgtgg 2600
 acggggtgca ggctttcttg cagacctatt cccacgaggt ttccctcacc 2650
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 catgctcgtc agccaggaga gctttgaaaa aagcgagccc cttttgctgt 2750
 caggtgattc ggtatcttct aaagacagtc atgggttaat tgaggtgagt 2800
 ttatatcaaa tottctttct tttttttttt aattgctctg tctccaagc 2850
 tggagtgcag cggtacgac atagctcact gcggcctcaa actcctaggc 2900
 tcaagcaatt atcccacctt tgctccgggt gtaacaggga ctacaggtgc 2950
 aagccaccta ctgtctgcct atctatctat ctatctatct atctatctat 3000
 ctatctatct atctatctat tactttcttg tacagacggg agtctcacgc 3050
 ctgtaatccc agtactttgg gaggccgagg cgggtggatc acctgagggt 3100
 gggagtttga gaccagcctg accaacaatgg agaaaccccg tctatactaa 3150
 aaaaatacaa aattagccgg gcgtgggtgt gcatgtctgt aatcccagct 3200
 acttgggagg ctgagtcagg agaattgctt taacctggga ggtggagggt 3250
 gcaatgagct gagattgtgc cattgcactc cagcctgggc aacaagagtg 3300
 aaactctatc tca 3313

<210> 390
 <211> 916
 <212> PRT
 <213> Homo sapiens
 <400> 390

Met	Ile	Pro	Ala	Arg	Leu	His	Arg	Asp	Tyr	Lys	Gly	Leu	Val	Leu	1	5	10	15
Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln	20	25	30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	275	280	285	
Asp	Lys	Ala	Ala	Gln	Val	Phe	Lys	Leu	Asp	Cys	Asn	Ser	Gly	Thr				

	290		295		300
Ile Ser Thr Ile	Gly 305	Glu Leu Asp His	Glu 310	Glu Ser Gly Phe	Tyr 315
Gln Met Glu Val	Gln 320	Ala Met Asp Asn	Ala 325	Gly Tyr Ser Ala	Arg 330
Ala Lys Val Leu	Ile 335	Thr Val Leu Asp	Val 340	Asn Asp Asn Ala	Pro 345
Glu Val Val Leu	Thr 350	Ser Leu Ala Ser	Ser 355	Val Pro Glu Asn	Ser 360
Pro Arg Gly Thr	Leu 365	Ile Ala Leu Leu	Asn 370	Val Asn Asp Gln	Asp 375
Ser Glu Glu Asn	Gly 380	Gln Val Ile Cys	Phe 385	Ile Gln Gly Asn	Leu 390
Pro Phe Lys Leu	Glu 395	Lys Ser Tyr Gly	Asn 400	Tyr Tyr Ser Leu	Val 405
Thr Asp Ile Val	Leu 410	Asp Arg Glu Gln	Val 415	Pro Ser Tyr Asn	Ile 420
Thr Val Thr Ala	Thr 425	Asp Arg Gly Thr	Pro 430	Pro Leu Ser Thr	Glu 435
Thr His Ile Ser	Leu 440	Asn Val Ala Asp	Thr 445	Asn Asp Asn Pro	Pro 450
Val Phe Pro Gln	Ala 455	Ser Tyr Ser Ala	Tyr 460	Ile Pro Glu Asn	Asn 465
Pro Arg Gly Val	Ser 470	Leu Val Ser Val	Thr 475	Ala His Asp Pro	Asp 480
Cys Glu Glu Asn	Ala 485	Gln Ile Thr Tyr	Ser 490	Leu Ala Glu Asn	Thr 495
Ile Gln Gly Ala	Ser 500	Leu Ser Ser Tyr	Val 505	Ser Ile Asn Ser	Asp 510
Thr Gly Val Leu	Tyr 515	Ala Leu Ser Ser	Phe 520	Asp Tyr Glu Gln	Phe 525
Arg Asp Leu Gln	Val 530	Lys Val Met Ala	Arg 535	Asp Asn Gly His	Pro 540
Pro Leu Ser Ser	Asn 545	Val Ser Leu Ser	Leu 550	Phe Val Leu Asp	Gln 555
Asn Asp Asn Ala	Pro 560	Glu Ile Leu Tyr	Pro 565	Ala Leu Pro Thr	Asp 570
Gly Ser Thr Gly	Val 575	Glu Leu Ala Pro	Arg 580	Ser Ala Glu Pro	Gly 585

Tyr	Leu	Val	Thr	Lys	Val	Val	Ala	Val	Asp	Arg	Asp	Ser	Gly	Gln	590	595	600
Asn	Ala	Trp	Leu	Ser	Tyr	Arg	Leu	Leu	Lys	Ala	Ser	Glu	Pro	Gly	605	610	615
Leu	Phe	Ser	Val	Gly	Leu	His	Thr	Gly	Glu	Val	Arg	Thr	Ala	Arg	620	625	630
Ala	Leu	Leu	Asp	Arg	Asp	Ala	Leu	Lys	Gln	Ser	Leu	Val	Val	Ala	635	640	645
Val	Gln	Asp	His	Gly	Gln	Pro	Pro	Leu	Ser	Ala	Thr	Val	Thr	Leu	650	655	660
Thr	Val	Ala	Val	Ala	Asp	Ser	Ile	Pro	Gln	Val	Leu	Ala	Asp	Leu	665	670	675
Gly	Ser	Leu	Glu	Ser	Pro	Ala	Asn	Ser	Glu	Thr	Ser	Asp	Leu	Thr	680	685	690
Leu	Tyr	Leu	Val	Val	Ala	Val	Ala	Ala	Val	Ser	Cys	Val	Phe	Leu	695	700	705
Ala	Phe	Val	Ile	Leu	Leu	Leu	Ala	Leu	Arg	Leu	Arg	Arg	Trp	His	710	715	720
Lys	Ser	Arg	Leu	Leu	Gln	Ala	Ser	Gly	Gly	Gly	Leu	Thr	Gly	Ala	725	730	735
Pro	Ala	Ser	His	Phe	Val	Gly	Val	Asp	Gly	Val	Gln	Ala	Phe	Leu	740	745	750
Gln	Thr	Tyr	Ser	His	Glu	Val	Ser	Leu	Thr	Thr	Asp	Ser	Arg	Lys	755	760	765
Ser	His	Leu	Ile	Phe	Pro	Gln	Pro	Asn	Tyr	Ala	Asp	Met	Leu	Val	770	775	780
Ser	Gln	Glu	Ser	Phe	Glu	Lys	Ser	Glu	Pro	Leu	Leu	Leu	Ser	Gly	785	790	795
Asp	Ser	Val	Phe	Ser	Lys	Asp	Ser	His	Gly	Leu	Ile	Glu	Val	Ser	800	805	810
Leu	Tyr	Gln	Ile	Phe	Phe	Leu	Phe	Phe	Phe	Asn	Cys	Ser	Val	Ser	815	820	825
Gln	Ala	Gly	Val	Gln	Arg	Tyr	Asp	His	Ser	Ser	Leu	Arg	Pro	Gln	830	835	840
Thr	Pro	Arg	Leu	Lys	Gln	Leu	Ser	His	Leu	Cys	Leu	Arg	Cys	Asn	845	850	855
Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr	860	865	870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu			

	875		880		885
Ser Cys Thr Asp	Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp				
	890		895		900
Glu Ala Glu Ala	Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro				
	905		910		915

Ala

<210> 391
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 391
 tccgtctctg tgaaccgccc cac 23

<210> 392
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 392
 ctcgggcgca ttgtcgttct ggtc 24

<210> 393
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 393
 ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394
 <211> 999
 <212> DNA
 <213> Homo sapiens

<400> 394
 cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50
 cccagttaaa aggtccaga atcgtgtacc aggcagagaa ctgaagtact 100
 ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150
 ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200

gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250
aggaggacaa ggtgctgggg ggtcatgagt gccaaaccca ttcgcagcct 300
tggcaggcgg ccttggtcca gggccagcaa ctactctgtg gcggtgtcct 350
tgtaggtggc aactgggtcc ttacagctgc ccactgtaaa aaaccgaaat 400
acacagtacg cctgggagac cacagcctac agaataaaga tggcccagag 450
caagaaatac ctgtggttca gtccatccca caccctgtct acaacagcag 500
cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgcgtgacc 550
aggcatccct ggggtccaaa gtgaagccca tcagcctggc agatcattgc 600
accagcctg gccagaagtg caccgtctca ggctggggca ctgtcaccag 650
tccccgagag aattttcctg acactctcaa ctgtgcagaa gtaaaaatct 700
ttccccagaa gaagtgtgag gatgcttacc cggggcagat cacagatggc 750
atgggtctgtg caggcagcag caaaggggct gacacgtgcc agggcgattc 800
tggaggcccc ctggtgtgtg atggtgcact ccagggcata acatcctggg 850
gctcagaccc ctgtgggagg tccgacaaac ctggcgtcta taccaacatc 900
tgccgctacc tggactggat caagaagatc ataggcagca agggctgatt 950
ctaggataag cactagatct cccttaataa actcacaact ctctggttc 999

<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met Gly Arg Pro Arg Pro Arg Ala Ala Lys Thr Trp Met Phe Leu
1 5 10 15

Leu Leu Leu Gly Gly Ala Trp Ala Gly His Ser Arg Ala Gln Glu
20 25 30

Asp Lys Val Leu Gly Gly His Glu Cys Gln Pro His Ser Gln Pro
35 40 45

Trp Gln Ala Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly
50 55 60

Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys
65 70 75

Lys Pro Lys Tyr Thr Val Arg Leu Gly Asp His Ser Leu Gln Asn
80 85 90

Lys Asp Gly Pro Glu Gln Glu Ile Pro Val Val Gln Ser Ile Pro
95 100 105

His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp
				110					115					120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys
				125					130					135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln
				140					145					150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu
				155					160					165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro
				170					175					180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly
				185					190					195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly
				200					205					210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile
				215					220					225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly
				230					235					240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile
				245					250					255
Ile	Gly	Ser	Lys	Gly										
				260										

<210> 396
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 396
 cagcctacag aataaagatg gccc 24

 <210> 397
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 397
 ggtgcaatga tctgccaggc tgat 24

 <210> 398
 <211> 48
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

ggcgccggtg caccgggagg gctgagcgcc tctgcgggcc cggcctgcgc 50
 gccccggccc gccgagccgc ccacgcccc accccggccc gcgcccccta 100
 gccccgccc gggcccgccg ccgagcccg gccaggtga gcgctccgcc 150
 cgccgcgagg ccccgccccg gcccgcccc gccccgccc ggccggcggg 200
 ggaaccgggc ggattcctcg cgggtcaaac cacctgatcc cataaaacat 250
 tcacctccc ggcgcccgcc gctgagagcg ccccgccagt ccgagccgcc 300
 gccgcccctg cctgtgcgc cctgagcgcc ctgagcacc gcggcccag 350
 cccagccaga gccgggagg gaggagcgcg ccgagcctcg tcccgcgcc 400
 gggccggggc cgggcccgtg cggcgcgcc tggtatgcga cccggccgcg 450
 gggagacggg cgcccgcccc gaaacgaatt tcagtcccc acgcgccccg 500
 cccaaccct acgatgaaga gggcgccgc tggagggagc cggctgctgg 550
 catgggtgct gtggctgcag gcctggcagg tggcagcccc atgccaggt 600
 gcctgcgtat gctacaatga gcccaagggt acgacaagct gccccagca 650
 gggcctgcag gctgtgccc tgggcatccc tgctgccagc cagcgcatct 700
 tctgcacgg caaccgcac tcgcatgtgc cagctgccag cttccgtgcc 750
 tgccgcaacc tcaccatcct gtggctgcac tcgaatgtgc tggcccgaat 800
 tgatgcggct gccttactg gcctggccct cctggagcag ctggacctca 850
 gcgataatgc acagctccg tctgtggacc ctgccacatt ccacggcctg 900
 ggccgcctac acacgctgca cctggaccgc tcgggcctgc aggagctggg 950
 cccggggctg ttccgcggcc tggctgccct gcagtacctc tacctgcagg 1000
 acaacgcgct gcaggcactg cctgatgaca ccttccgcga cctgggcaac 1050
 ctcacacacc tcttctgca cggcaaccgc atctccagcg tgcccgagcg 1100

cgcttccgt gggctgcaca gcctcgaccg tctctactg caccagaacc 1150
 gctgggcca tgtgcacccg catgccttcc gtgaccttg cgcctcatg 1200
 acactctatc tgtttgcca caatctatca gcgctgcca ctgaggccct 1250
 ggccccctg cgtgccctgc agtacctgag gctcaacgac aaccctggg 1300
 tgtgtgactg ccgggcacgc ccaactctggg cctggctgca gaagttccgc 1350
 ggctcctcct ccgaggtgcc ctgcagcctc ccgcaacgcc tggctggccg 1400
 tgacctcaaa cgcttagctg ccaatgacct gcagggctgc gctgtggcca 1450
 ccggccctta ccatcccatc tggaccggca gggccaccga tgaggagccg 1500
 ctggggcttc ccaagtgcctg ccagccagat gccgctgaca aggcctcagt 1550
 actggagcct ggaagaccag cttcggcagg caatgcgctg aaggacgcg 1600
 tgccgcccgg tgacagcccg ccgggcaacg gctctggccc acggcacatc 1650
 aatgactcac cctttgggac tctgcctggc tctgctgagc ccccgctcac 1700
 tgcagtgcgg cccgagggct ccgagccacc agggttcccc acctcgggcc 1750
 ctcgccggag gccaggctgt tcacgcaaga accgcacccg cagccactgc 1800
 cgtctgggcc aggcaggcag cgggggtggc gggactggtg actcagaagg 1850
 ctcaggtgcc ctaccagacc tcacctgcag cctcaccccc ctgggcctgg 1900
 cgctggtgct gtggacagtg cttgggccct gctgaccccc agcggacaca 1950
 agagcgtgct cagcagccag gtgtgtgtac atacggggtc tctctccacg 2000
 ccgccaagcc agccgggcgg ccgaccctg gggcaggcca ggccaggtcc 2050
 tccctgatgg acgcctgccg cccgccaccc ccatctccac cccatcatgt 2100
 ttacaggggt cggcggcagc gtttggtcca gaacgccgcc tcccaccag 2150
 atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200
 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400
 <211> 473
 <212> PRT
 <213> Homo sapiens

<400> 400
 Met Lys Arg Ala Ser Ala Gly Gly Ser Arg Leu Leu Ala Trp Val
 1 5 10 15
 Leu Trp Leu Gln Ala Trp Gln Val Ala Ala Pro Cys Pro Gly Ala
 20 25 30

Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln
				35					40					45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln
				50					55					60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala
				65					70					75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser
				80					85					90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala
				95					100					105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser
				110					115					120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu
				125					130					135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe
				140					145					150
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala
				155					160					165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu
				170					175					180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu
				185					190					195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His
				200					205					210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu
				215					220					225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala
				230					235					240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu
				245					250					255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro
				260					265					270
Leu	Trp	Ala	Trp	Leu	Gln	Lys	Phe	Arg	Gly	Ser	Ser	Ser	Glu	Val
				275					280					285
Pro	Cys	Ser	Leu	Pro	Gln	Arg	Leu	Ala	Gly	Arg	Asp	Leu	Lys	Arg
				290					295					300
Leu	Ala	Ala	Asn	Asp	Leu	Gln	Gly	Cys	Ala	Val	Ala	Thr	Gly	Pro
				305					310					315
Tyr	His	Pro	Ile	Trp	Thr	Gly	Arg	Ala	Thr	Asp	Glu	Glu	Pro	Leu

320	325	330
Gly Leu Pro Lys Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala Ser	
335	340	345
Val Leu Glu Pro Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu Lys	
350	355	360
Gly Arg Val Pro Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser Gly	
365	370	375
Pro Arg His Ile Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly Ser	
380	385	390
Ala Glu Pro Pro Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu Pro	
395	400	405
Pro Gly Phe Pro Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys Ser	
410	415	420
Arg Lys Asn Arg Thr Arg Ser His Cys	Arg Leu Gly Gln Ala Gly	
425	430	435
Ser Gly Gly Gly Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala Leu	
440	445	450
Pro Ser Leu Thr Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu Val	
455	460	465
Leu Trp Thr Val Leu Gly Pro Cys		
470		

<210> 401
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 401
 tggctgccct gcagtacctc tacc 24

<210> 402
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 402
 ccctgcaggt cattggcagc tagg 24

<210> 403
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

ggaagtccac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50
ggagaggact actcactggc atatttctga ggtatctgta gaataaccac 100
agcctcagat actggggact ttacagtccc acagaaccgt cctcccagga 150
agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200
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<210> 405
 <211> 798
 <212> PRT
 <213> Homo sapiens

<400> 405

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Pro	Arg	Ser	Tyr	Ser	Val	Val	Glu	Glu	Thr	Glu	Gly	Ser	Ser	Phe
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Val	Thr	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Leu	Glu	Gln	Arg	Glu	Phe
			50						55					60
Ser	Arg	Arg	Gly	Val	Arg	Val	Val	Ser	Arg	Gly	Asn	Lys	Leu	His
			65						70					75
Leu	Gln	Leu	Asn	Gln	Glu	Thr	Ala	Asp	Leu	Leu	Leu	Asn	Glu	Lys
			80						85					90
Leu	Asp	Arg	Glu	Asp	Leu	Cys	Gly	His	Thr	Glu	Pro	Cys	Val	Leu
			95						100					105
Arg	Phe	Gln	Val	Leu	Leu	Glu	Ser	Pro	Phe	Glu	Phe	Phe	Gln	Ala
			110						115					120
Glu	Leu	Gln	Val	Ile	Asp	Ile	Asn	Asp	His	Ser	Pro	Val	Phe	Leu
			125						130					135
Asp	Lys	Gln	Met	Leu	Val	Lys	Val	Ser	Glu	Ser	Ser	Pro	Pro	Gly
			140						145					150
Thr	Thr	Phe	Pro	Leu	Lys	Asn	Ala	Glu	Asp	Leu	Asp	Val	Gly	Gln
			155						160					165
Asn	Asn	Ile	Glu	Asn	Tyr	Ile	Ile	Ser	Pro	Asn	Ser	Tyr	Phe	Arg
			170						175					180
Val	Leu	Thr	Arg	Lys	Arg	Ser	Asp	Gly	Arg	Lys	Tyr	Pro	Glu	Leu
			185						190					195
Val	Leu	Asp	Lys	Ala	Leu	Asp	Arg	Glu	Glu	Glu	Ala	Glu	Leu	Arg
			200						205					210
Leu	Thr	Leu	Thr	Ala	Leu	Asp	Gly	Gly	Ser	Pro	Pro	Arg	Ser	Gly
			215						220					225
Thr	Ala	Gln	Val	Tyr	Ile	Glu	Val	Leu	Asp	Val	Asn	Asp	Asn	Ala

230	235	240
Pro Glu Phe Glu Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp		
245	250	255
Ser Pro Val Gly Phe Leu Val Val Lys Val Ser Ala Thr Asp Val		
260	265	270
Asp Thr Gly Val Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala		
275	280	285
Ser Glu Glu Ile Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly		
290	295	300
Glu Ile Glu Leu Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser		
305	310	315
Tyr Glu Val Asn Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly		
320	325	330
Lys Cys Thr Val Leu Ile Gln Val Ile Asp Val Asn Asp His Ala		
335	340	345
Pro Glu Val Thr Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn		
350	355	360
Ala Pro Glu Thr Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp		
365	370	375
Ser Gly Glu Asn Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu		
380	385	390
Pro Phe Leu Leu Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr		
395	400	405
Glu Arg Pro Leu Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr		
410	415	420
Ile Thr Val Thr Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu		
425	430	435
Asn Met Thr Val Leu Ile Ala Asp Val Asn Asp Asn Ala Pro Ala		
440	445	450
Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser		
455	460	465
Pro Ala Leu His Ile Arg Ser Val Ser Ala Thr Asp Arg Asp Ser		
470	475	480
Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp		
485	490	495
Pro His Leu Pro Leu Thr Ser Leu Val Ser Ile Asn Ala Asp Asn		
500	505	510
Gly His Leu Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln		
515	520	525

Gly	Phe	Gln	Phe	Arg	Val	Gly	Ala	Ser	Asp	His	Gly	Ser	Pro	Ala	
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				545					550					555	
Asp	Asn	Ser	Pro	Phe	Val	Leu	Tyr	Pro	Leu	Gln	Asn	Gly	Ser	Ala	
				560					565					570	
Pro	Cys	Thr	Glu	Leu	Val	Pro	Arg	Ala	Ala	Glu	Pro	Gly	Tyr	Leu	
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Val	Thr	Lys	Val	Val	Ala	Val	Asp	Gly	Asp	Ser	Gly	Gln	Asn	Ala	
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Trp	Leu	Ser	Tyr	Gln	Leu	Leu	Lys	Ala	Thr	Glu	Leu	Gly	Leu	Phe	
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Gly	Val	Trp	Ala	His	Asn	Gly	Glu	Val	Arg	Thr	Ala	Arg	Leu	Leu	
				620					625					630	
Ser	Glu	Arg	Asp	Ala	Ala	Lys	His	Arg	Leu	Val	Val	Leu	Val	Lys	
				635					640					645	
Asp	Asn	Gly	Glu	Pro	Pro	Arg	Ser	Ala	Thr	Ala	Thr	Leu	His	Val	
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Leu	Leu	Val	Asp	Gly	Phe	Ser	Gln	Pro	Tyr	Leu	Pro	Leu	Pro	Glu	
				665					670					675	
Ala	Ala	Pro	Thr	Gln	Ala	Gln	Ala	Asp	Leu	Leu	Thr	Val	Tyr	Leu	
				680					685					690	
Val	Val	Ala	Leu	Ala	Ser	Val	Ser	Ser	Leu	Phe	Leu	Phe	Ser	Val	
				695					700					705	
Leu	Leu	Phe	Val	Ala	Val	Arg	Leu	Cys	Arg	Arg	Ser	Arg	Ala	Ala	
				710					715					720	
Ser	Val	Gly	Arg	Cys	Leu	Val	Pro	Glu	Gly	Pro	Leu	Pro	Gly	His	
				725					730					735	
Leu	Val	Asp	Met	Ser	Gly	Thr	Arg	Thr	Leu	Ser	Gln	Ser	Tyr	Gln	
				740					745					750	
Tyr	Glu	Val	Cys	Leu	Ala	Gly	Gly	Ser	Gly	Thr	Asn	Glu	Phe	Lys	
				755					760					765	
Phe	Leu	Lys	Pro	Ile	Ile	Pro	Asn	Phe	Pro	Pro	Gln	Cys	Pro	Gly	
				770					775					780	
Lys	Glu	Ile	Gln	Gly	Asn	Ser	Thr	Phe	Pro	Asn	Asn	Phe	Gly	Phe	
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<210> 406

<211> 23
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 407
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 407
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<210> 408
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 409
 <211> 1379
 <212> DNA
 <213> Homo sapiens

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 cggtcgacga ccgccccgcg tcatgoggct cctcggctgg tggcaagtat 150
 tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200
 agtggctcgt tatggtcaga ggagcagcct gctcaccctc tccaggtggg 250
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 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400
 gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450
 caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500

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<210> 410
<211> 360
<212> PRT
<213> Homo sapiens

<400> 410
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35 40 45
Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly
50 55 60
Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala
65 70 75
Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His

				80					85					90
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Ser	Ser	Glu	Pro	Ser 110	Gly	Val	Thr	Cys	Gly 115	Ala	Gly	Gly	Ala	Glu 120
Asp	Ser	Arg	Cys	Asn 125	Val	Arg	Glu	Ser	Leu 130	Phe	Ser	Leu	Asp	Gly 135
Ala	Gly	Ala	His	Phe 140	Pro	Asp	Arg	Glu	Glu 145	Glu	Tyr	Tyr	Thr	Glu 150
Pro	Glu	Val	Ala	Glu 155	Ser	Asp	Ala	Ala	Pro 160	Thr	Glu	Asp	Ser	Asn 165
Asn	Thr	Glu	Ser	Leu 170	Lys	Ser	Pro	Lys	Val 175	Asn	Cys	Glu	Glu	Arg 180
Asn	Ile	Thr	Gly	Leu 185	Glu	Asn	Phe	Thr	Leu 190	Lys	Ile	Leu	Asn	Met 195
Ser	Gln	Asp	Leu	Met 200	Asp	Phe	Leu	Asn	Pro 205	Asn	Gly	Ser	Asp	Cys 210
Thr	Leu	Val	Leu	Phe 215	Tyr	Thr	Pro	Trp	Cys 220	Arg	Phe	Ser	Ala	Ser 225
Leu	Ala	Pro	His	Phe 230	Asn	Ser	Leu	Pro	Arg 235	Ala	Phe	Pro	Ala	Leu 240
His	Phe	Leu	Ala	Leu 245	Asp	Ala	Ser	Gln	His 250	Ser	Ser	Leu	Ser	Thr 255
Arg	Phe	Gly	Thr	Val 260	Ala	Val	Pro	Asn	Ile 265	Leu	Leu	Phe	Gln	Gly 270
Ala	Lys	Pro	Met	Ala 275	Arg	Phe	Asn	His	Thr 280	Asp	Arg	Thr	Leu	Glu 285
Thr	Leu	Lys	Ile	Phe 290	Ile	Phe	Asn	Gln	Thr 295	Gly	Ile	Glu	Ala	Lys 300
Lys	Asn	Val	Val	Val 305	Thr	Gln	Ala	Asp	Gln 310	Ile	Gly	Pro	Leu	Pro 315
Ser	Thr	Leu	Ile	Lys 320	Ser	Val	Asp	Trp	Leu 325	Leu	Val	Phe	Ser	Leu 330
Phe	Phe	Leu	Ile	Ser 335	Phe	Ile	Met	Tyr	Ala 340	Thr	Ile	Arg	Thr	Glu 345
Ser	Ile	Arg	Trp	Leu 350	Ile	Pro	Gly	Gln	Glu 355	Gln	Glu	His	Val	Glu 360

278

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 411
cacagagcca gaagtggcgg aatc 24

<210> 412
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 412
ccacatgttc ctgctcttgc cctgg 25

<210> 413
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 413
cggtagtgac tgtactctag tctgtttta caccctgtgg tgccg 45

<210> 414
<211> 1196
<212> DNA
<213> Homo sapiens

<400> 414
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Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	Leu	Leu	Pro	Ala	Thr	
				155					160					165	
Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys	Asn	Lys	Asn	Asp	
				170					175					180	
Asp	Asp	Asn	Asp	Ile	Met	Glu	Thr	Leu	Cys	Lys	Asn	Asp	Phe	Ala	
				185					190					195	
Leu	Lys	Ile	Lys	Val	Lys	Glu	Ile	Thr	Tyr	Ile	Asn	Arg	Asp	Thr	
				200					205					210	
Lys	Ile	Ile	Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	Asn	
				215					220					225	
Gly	Val	Ser	Glu	Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	
				230					235					240	
Asp	Ser	Leu	Gln	Cys	Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	
				245					250					255	
Pro	Tyr	Leu	Val	Met	Gly	Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	
				260					265					270	
Thr	Ser	Val	Lys	Arg	Trp	Gln	Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	
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<210> 416
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 416
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<210> 417
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 417
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<210> 418
 <211> 47
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

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<210> 419

<211> 1830

<212> DNA

<213> Homo sapiens

<400> 419

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 cccggctggg tctcactcct ccttctcctc cccgtgggtg atcacgtagc 1700
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<210> 420

<211> 560

<212> PRT

<213> Homo sapiens

<400> 420

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Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr
			35						40					45
Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp
			50						55					60
Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr
			65						70					75
Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu
			80						85					90
Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu
			95						100					105
Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val

				110						115					120
Gly	Thr	Gln	Asn	Pro	Phe	Ala	Phe	Leu	Met	Gly	Gly	Gln	Ser	Leu	
				125					130					135	
Cys	Ala	Leu	Ala	Gln	Ser	Leu	Val	Ile	Phe	Ser	Pro	Ala	Lys	Leu	
				140					145					150	
Ala	Ala	Leu	Trp	Phe	Pro	Glu	His	Gln	Arg	Ala	Thr	Ala	Asn	Met	
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Leu	Ala	Thr	Met	Ser	Asn	Pro	Leu	Gly	Val	Leu	Val	Ala	Asn	Val	
				170					175					180	
Leu	Ser	Pro	Val	Leu	Val	Lys	Lys	Gly	Glu	Asp	Ile	Pro	Leu	Met	
				185					190					195	
Leu	Gly	Val	Tyr	Thr	Ile	Pro	Ala	Gly	Val	Val	Cys	Leu	Leu	Ser	
				200					205					210	
Thr	Ile	Cys	Leu	Trp	Glu	Ser	Val	Pro	Pro	Thr	Pro	Pro	Ser	Ala	
				215					220					225	
Gly	Ala	Ala	Ser	Ser	Thr	Ser	Glu	Lys	Phe	Leu	Asp	Gly	Leu	Lys	
				230					235					240	
Leu	Gln	Leu	Met	Trp	Asn	Lys	Ala	Tyr	Val	Ile	Leu	Ala	Val	Cys	
				245					250					255	
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Glu	Gln	Ile	Leu	Cys	Ala	Ser	Gly	His	Ser	Ser	Gly	Phe	Ser	Gly	
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Leu	Cys	Gly	Ala	Leu	Phe	Ile	Thr	Phe	Gly	Ile	Leu	Gly	Ala	Leu	
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Ala	Ala	Thr	Gly	Met	Ile	Phe	Val	Leu	Gly	Gln	Ala	Glu	Gly	Ile	
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Leu	Ile	Met	Leu	Ala	Met	Thr	Ala	Leu	Thr	Val	Arg	Arg	Ser	Glu	
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Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu Asp Trp
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Thr Val Ser Leu Leu Leu Met Ala Gly Leu Cys Thr Phe Phe Ser
425 430 435

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440 445 450

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455 460 465

Ala Asp Ser Gly Pro Gly Val Asp Arg Gly Gly Ala Gly Arg Ala
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Gly Val Leu Gly Pro Ser Thr Ala Thr Pro Glu Cys Thr Ala Arg
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Gly Ala Ser Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro
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Ala Cys His Arg Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr
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Asp Ala Pro Ser Arg Pro Gly Arg Leu Ala Gly Arg Val Gln Ala
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Pro Trp Val Ile Thr
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<220>
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<400> 422
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<400> 423

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<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

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<210> 425
 <211> 1184
 <212> PRT
 <213> Homo sapiens

<400> 425
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 Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val
 35 40 45
 Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg
 50 55 60
 Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu
 65 70 75
 Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg
 80 85 90
 Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu
 95 100 105
 Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His
 110 115 120
 Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe
 125 130 135
 Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu
 140 145 150
 Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly
 155 160 165
 Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe
 170 175 180
 Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu
 185 190 195

Leu Ile Val Val	Lys Glu Leu Asp Arg	Glu Ile His Ser Phe Phe	200	205	210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn Gly	Asn Pro Pro Lys Ser	215	220	225
Gly Thr Ser Leu	Val Lys Val Asn Val	Leu Asp Ser Asn Asp Asn	230	235	240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu	Ala Leu Glu Ile Gln Glu	245	250	255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile	Lys Leu Thr Ala Thr Asp	260	265	270
Pro Asp Gln Gly	Pro Asn Gly Glu Val	Glu Phe Phe Leu Ser Lys	275	280	285
His Met Pro Pro	Glu Val Leu Asp Thr	Phe Ser Ile Asp Ala Lys	290	295	300
Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys Asn	305	310	315
Pro Ala Tyr Glu	Val Asp Val Gln Ala	Arg Asp Leu Gly Pro Asn	320	325	330
Pro Ile Pro Ala	His Cys Lys Val Leu	Ile Lys Val Leu Asp Val	335	340	345
Asn Asp Asn Ile	Pro Ser Ile His Val	Thr Trp Ala Ser Gln Pro	350	355	360
Ser Leu Val Ser	Glu Ala Leu Pro Lys	Asp Ser Phe Ile Ala Leu	365	370	375
Val Met Ala Asp	Asp Leu Asp Ser Gly	His Asn Gly Leu Val His	380	385	390
Cys Trp Leu Ser	Gln Glu Leu Gly His	Phe Arg Leu Lys Arg Thr	395	400	405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr	Asn Ala Thr Leu Asp Arg	410	415	420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr	Leu Leu Ala Gln Asp Gln	425	430	435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys	Gln Leu Ser Ile Gln Ile	440	445	450
Ser Asp Ile Asn	Asp Asn Ala Pro Val	Phe Glu Lys Ser Arg Tyr	455	460	465
Glu Val Ser Thr	Arg Glu Asn Asn Leu	Pro Ser Leu His Leu Ile	470	475	480
Thr Ile Lys Ala	His Asp Ala Asp Leu	Gly Ile Asn Gly Lys Val			

	485		490		495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val	Ala His Leu Val Ala	Ile		
	500	505	510		
Asp Ser Asn Thr	Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn	Tyr		
	515	520	525		
Glu Glu Met Ala	Gly Phe Glu Phe Gln	Val Ile Ala Glu Asp	Ser		
	530	535	540		
Gly Gln Pro Met	Leu Ala Ser Ser Val	Ser Val Trp Val Ser	Leu		
	545	550	555		
Leu Asp Ala Asn	Asp Asn Ala Pro Glu	Val Val Gln Pro Val	Leu		
	560	565	570		
Ser Asp Gly Lys	Ala Ser Leu Ser Val	Leu Val Asn Ala Ser	Thr		
	575	580	585		
Gly His Leu Leu	Val Pro Ile Glu Thr	Pro Asn Gly Leu Gly	Pro		
	590	595	600		
Ala Gly Thr Asp	Thr Pro Pro Leu Ala	Thr His Ser Ser Arg	Pro		
	605	610	615		
Phe Leu Leu Thr	Thr Ile Val Ala Arg	Asp Ala Asp Ser Gly	Ala		
	620	625	630		
Asn Gly Glu Pro	Leu Tyr Ser Ile Arg	Asn Gly Asn Glu Ala	His		
	635	640	645		
Leu Phe Ile Leu	Asn Pro His Thr Gly	Gln Leu Phe Val Asn	Val		
	650	655	660		
Thr Asn Ala Ser	Ser Leu Ile Gly Ser	Glu Trp Glu Leu Glu	Ile		
	665	670	675		
Val Val Glu Asp	Gln Gly Ser Pro Pro	Leu Gln Thr Arg Ala	Leu		
	680	685	690		
Leu Arg Val Met	Phe Val Thr Ser Val	Asp His Leu Arg Asp	Ser		
	695	700	705		
Ala Arg Lys Pro	Gly Ala Leu Ser Met	Ser Met Leu Thr Val	Ile		
	710	715	720		
Cys Leu Ala Val	Leu Leu Gly Ile Phe	Gly Leu Ile Leu Ala	Leu		
	725	730	735		
Phe Met Ser Ile	Cys Arg Thr Glu Lys	Lys Asp Asn Arg Ala	Tyr		
	740	745	750		
Asn Cys Arg Glu	Ala Glu Ser Thr Tyr	Arg Gln Gln Pro Lys	Arg		
	755	760	765		
Pro Gln Lys His	Ile Gln Lys Ala Asp	Ile His Leu Val Pro	Val		
	770	775	780		

Leu	Arg	Gly	Gln	Ala	Gly	Glu	Pro	Cys	Glu	Val	Gly	Gln	Ser	His
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Lys	Asp	Val	Asp	Lys	Glu	Ala	Met	Met	Glu	Ala	Gly	Trp	Asp	Pro
				800					805					810
Cys	Leu	Gln	Ala	Pro	Phe	His	Leu	Thr	Pro	Thr	Leu	Tyr	Arg	Thr
				815					820					825
Leu	Arg	Asn	Gln	Gly	Asn	Gln	Gly	Ala	Pro	Ala	Glu	Ser	Arg	Glu
				830					835					840
Val	Leu	Gln	Asp	Thr	Val	Asn	Leu	Leu	Phe	Asn	His	Pro	Arg	Gln
				845					850					855
Arg	Asn	Ala	Ser	Arg	Glu	Asn	Leu	Asn	Leu	Pro	Glu	Pro	Gln	Pro
				860					865					870
Ala	Thr	Gly	Gln	Pro	Arg	Ser	Arg	Pro	Leu	Lys	Val	Ala	Gly	Ser
				875					880					885
Pro	Thr	Gly	Arg	Leu	Ala	Gly	Asp	Gln	Gly	Ser	Glu	Glu	Ala	Pro
				890					895					900
Gln	Arg	Pro	Pro	Ala	Ser	Ser	Ala	Thr	Leu	Arg	Arg	Gln	Arg	His
				905					910					915
Leu	Asn	Gly	Lys	Val	Ser	Pro	Glu	Lys	Glu	Ser	Gly	Pro	Arg	Gln
				920					925					930
Ile	Leu	Arg	Ser	Leu	Val	Arg	Leu	Ser	Val	Ala	Ala	Phe	Ala	Glu
				935					940					945
Arg	Asn	Pro	Val	Glu	Glu	Leu	Thr	Val	Asp	Ser	Pro	Pro	Val	Gln
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Gln	Ile	Ser	Gln	Leu	Leu	Ser	Leu	Leu	His	Gln	Gly	Gln	Phe	Gln
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Pro	Lys	Pro	Asn	His	Arg	Gly	Asn	Lys	Tyr	Leu	Ala	Lys	Pro	Gly
				980					985					990
Gly	Ser	Arg	Ser	Ala	Ile	Pro	Asp	Thr	Asp	Gly	Pro	Ser	Ala	Arg
				995					1000					1005
Ala	Gly	Gly	Gln	Thr	Asp	Pro	Glu	Gln	Glu	Glu	Gly	Pro	Leu	Asp
				1010					1015					1020
Pro	Glu	Glu	Asp	Leu	Ser	Val	Lys	Gln	Leu	Leu	Glu	Glu	Glu	Leu
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Ser	Ser	Leu	Leu	Asp	Pro	Ser	Thr	Gly	Leu	Ala	Leu	Asp	Arg	Leu
				1040					1045					1050
Ser	Ala	Pro	Asp	Pro	Ala	Trp	Met	Ala	Arg	Leu	Ser	Leu	Pro	Leu
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Thr	Thr	Asn	Tyr	Arg	Asp	Asn	Val	Ile	Ser	Pro	Asp	Ala	Ala	Ala

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Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala		
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Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val		
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Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser		
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Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser		
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Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala		
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<210> 427
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 427
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<210> 428
 <211> 50
 <212> DNA
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<400> 428
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<210> 429
 <211> 2037

<212> DNA
<213> Homo sapiens

<400> 429

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<210> 430

<211> 455

<212> PRT

<213> Homo sapiens

<400> 430

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			20						25					30
Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser
			35						40					45
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe
			50						55					60
Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp
			65						70					75
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val
			80						85					90
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu
			95						100					105
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe
			110						115					120

Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser	125	130	135
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val	140	145	150
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly	155	160	165
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn	170	175	180
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln	185	190	195
Thr	Met	Asp	Met	Ile	Ile	Ser	Lys	Lys	Lys	Arg	Met	Ala	Met	Ala	200	205	210
Arg	Arg	Thr	Met	Phe	Gln	Lys	Gly	Glu	Val	His	Asn	Lys	Pro	Ser	215	220	225
Gly	Phe	Trp	Gly	Met	Ile	Lys	Ser	Val	Thr	Thr	Ser	Ala	Ser	Gly	230	235	240
Ser	Glu	Asn	Leu	Thr	Leu	Ile	Gln	Gln	Glu	Val	Asp	Ala	Leu	Glu	245	250	255
Glu	Leu	Ser	Arg	Gln	Leu	Phe	Leu	Glu	Thr	Ala	Asp	Leu	Tyr	Ala	260	265	270
Thr	Lys	Glu	Arg	Ile	Glu	Tyr	Ser	Lys	Thr	Phe	Lys	Gly	Lys	Tyr	275	280	285
Phe	Asn	Phe	Leu	Gly	Tyr	Phe	Phe	Ser	Ile	Tyr	Cys	Val	Trp	Lys	290	295	300
Ile	Phe	Met	Ala	Thr	Ile	Asn	Ile	Val	Phe	Asp	Arg	Val	Gly	Lys	305	310	315
Thr	Asp	Pro	Val	Thr	Arg	Gly	Ile	Glu	Ile	Thr	Val	Asn	Tyr	Leu	320	325	330
Gly	Ile	Gln	Phe	Asp	Val	Lys	Phe	Trp	Ser	Gln	His	Ile	Ser	Phe	335	340	345
Ile	Leu	Val	Gly	Ile	Ile	Ile	Val	Thr	Ser	Ile	Arg	Gly	Leu	Leu	350	355	360
Ile	Thr	Leu	Thr	Lys	Phe	Phe	Tyr	Ala	Ile	Ser	Ser	Ser	Lys	Ser	365	370	375
Ser	Asn	Val	Ile	Val	Leu	Leu	Leu	Ala	Gln	Ile	Met	Gly	Met	Tyr	380	385	390
Phe	Val	Ser	Ser	Val	Leu	Leu	Ile	Arg	Met	Ser	Met	Pro	Leu	Glu	395	400	405
Tyr	Arg	Thr	Ile	Ile	Thr	Glu	Val	Leu	Gly	Glu	Leu	Gln	Phe	Asn			

410	415	420
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Lys Gln Met Ala Pro		
455		

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 <213> Homo sapiens

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 <222> 78, 81, 113, 157, 224, 297
 <223> unknown base

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<210> 432
 <211> 457
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<220>
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 <222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
 <223> unknown base

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 tgagcaatat cggactactg cataaacaac gactgctttt ttcctgtctn 400
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<210> 434
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 <223> Synthetic oligonucleotide probe

<400> 434
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<210> 435
 <211> 41
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic oligonucleotide probe

<400> 435
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<210> 436
 <211> 3951
 <212> DNA
 <213> Homo sapiens

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a 3951

<210> 437

<211> 1141

<212> PRT

<213> Homo sapiens

<400> 437

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Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
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Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
				50					55					60

Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
				65					70					75

Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly
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80										85					90				
Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg					
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Val	Asp	Ile	Asp	Gln	Gly	Ala	Asp	Met	Gln	Lys	Glu	Ser	Lys	Glu					
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Asn	Gln	Trp	Leu	Gly	Val	Ser	Val	Arg	Ser	Gln	Gly	Pro	Gly	Gly					
				125					130					135					
Lys	Ile	Val	Thr	Cys	Ala	His	Arg	Tyr	Glu	Ala	Arg	Gln	Arg	Val					
				140					145					150					
Asp	Gln	Ile	Leu	Glu	Thr	Arg	Asp	Met	Ile	Gly	Arg	Cys	Phe	Val					
				155					160					165					
Leu	Ser	Gln	Asp	Leu	Ala	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Gly	Glu					
				170					175					180					
Trp	Lys	Phe	Cys	Glu	Gly	Arg	Pro	Gln	Gly	His	Glu	Gln	Phe	Gly					
				185					190					195					
Phe	Cys	Gln	Gln	Gly	Thr	Ala	Ala	Ala	Phe	Ser	Pro	Asp	Ser	His					
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Tyr	Leu	Leu	Phe	Gly	Ala	Pro	Gly	Thr	Tyr	Asn	Trp	Lys	Gly	Thr					
				215					220					225					
Ala	Arg	Val	Glu	Leu	Cys	Ala	Gln	Gly	Ser	Ala	Asp	Leu	Ala	His					
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Leu	Asp	Asp	Gly	Pro	Tyr	Glu	Ala	Gly	Gly	Glu	Lys	Glu	Gln	Asp					
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Pro	Arg	Leu	Ile	Pro	Val	Pro	Ala	Asn	Ser	Tyr	Phe	Gly	Phe	Ser					
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Ile	Asp	Ser	Gly	Lys	Gly	Leu	Val	Arg	Ala	Glu	Glu	Leu	Ser	Phe					
				275					280					285					
Val	Ala	Gly	Ala	Pro	Arg	Ala	Asn	His	Lys	Gly	Ala	Val	Val	Ile					
				290					295					300					
Leu	Arg	Lys	Asp	Ser	Ala	Ser	Arg	Leu	Val	Pro	Glu	Val	Met	Leu					
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Ser	Gly	Glu	Arg	Leu	Thr	Ser	Gly	Phe	Gly	Tyr	Ser	Leu	Ala	Val					
				320					325					330					
Ala	Asp	Leu	Asn	Ser	Asp	Gly	Trp	Pro	Asp	Leu	Ile	Val	Gly	Ala					
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Pro	Tyr	Phe	Phe	Glu	Arg	Gln	Glu	Glu	Leu	Gly	Gly	Ala	Val	Tyr					
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Val	Tyr	Leu	Asn	Gln	Gly	Gly	His	Trp	Ala	Gly	Ile	Ser	Pro	Leu					
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Arg	Leu	Cys	Gly	Ser	Pro	Asp	Ser	Met	Phe	Gly	Ile	Ser	Leu	Ala	
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Val	Leu	Gly	Asp	Leu	Asn	Gln	Asp	Gly	Phe	Pro	Asp	Ile	Ala	Val	
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Gly	Ala	Pro	Phe	Asp	Gly	Asp	Gly	Lys	Val	Phe	Ile	Tyr	His	Gly	
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Ser	Ser	Leu	Gly	Val	Val	Ala	Lys	Pro	Ser	Gln	Val	Leu	Glu	Gly	
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Glu	Ala	Val	Gly	Ile	Lys	Ser	Phe	Gly	Tyr	Ser	Leu	Ser	Gly	Ser	
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Leu	Asp	Met	Asp	Gly	Asn	Gln	Tyr	Pro	Asp	Leu	Leu	Val	Gly	Ser	
				455					460					465	
Leu	Ala	Asp	Thr	Ala	Val	Leu	Phe	Arg	Ala	Arg	Pro	Ile	Leu	His	
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Val	Ser	His	Glu	Val	Ser	Ile	Ala	Pro	Arg	Ser	Ile	Asp	Leu	Glu	
				485					490					495	
Gln	Pro	Asn	Cys	Ala	Gly	Gly	His	Ser	Val	Cys	Val	Asp	Leu	Arg	
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Val	Cys	Phe	Ser	Tyr	Ile	Ala	Val	Pro	Ser	Ser	Tyr	Ser	Pro	Thr	
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Val	Ala	Leu	Asp	Tyr	Val	Leu	Asp	Ala	Asp	Thr	Asp	Arg	Arg	Leu	
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Arg	Gly	Gln	Val	Pro	Arg	Val	Thr	Phe	Leu	Ser	Arg	Asn	Leu	Glu	
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Arg	Ala	Glu	Ile	His	Phe	Leu	Lys	Gln	Gly	Cys	Gly	Glu	Asp	Lys	
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Gln	Ala	Asp	Gly	Asp	Asp	Ala	His	Glu	Ala	Gln	Leu	Leu	Val	Met					
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Leu	Pro	Asp	Ser	Leu	His	Tyr	Ser	Gly	Val	Arg	Ala	Leu	Asp	Pro					
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				740					745					750					
Glu	Cys	Glu	Leu	Gly	Asn	Pro	Met	Lys	Arg	Gly	Ala	Gln	Val	Thr					
				755					760					765					
Phe	Tyr	Leu	Ile	Leu	Ser	Thr	Ser	Gly	Ile	Ser	Ile	Glu	Thr	Thr					
				770					775					780					
Glu	Leu	Glu	Val	Glu	Leu	Leu	Leu	Ala	Thr	Ile	Ser	Glu	Gln	Glu					
				785					790					795					
Leu	His	Pro	Val	Ser	Ala	Arg	Ala	Arg	Val	Phe	Ile	Glu	Leu	Pro					
				800					805					810					
Leu	Ser	Ile	Ala	Gly	Met	Ala	Ile	Pro	Gln	Gln	Leu	Phe	Phe	Ser					
				815					820					825					
Gly	Val	Val	Arg	Gly	Glu	Arg	Ala	Met	Gln	Ser	Glu	Arg	Asp	Val					
				830					835					840					
Gly	Ser	Lys	Val	Lys	Tyr	Glu	Val	Thr	Val	Ser	Asn	Gln	Gly	Gln					
				845					850					855					
Ser	Leu	Arg	Thr	Leu	Gly	Ser	Ala	Phe	Leu	Asn	Ile	Met	Trp	Pro					
				860					865					870					
His	Glu	Ile	Ala	Asn	Gly	Lys	Trp	Leu	Leu	Tyr	Pro	Met	Gln	Val					
				875					880					885					
Glu	Leu	Glu	Gly	Gly	Gln	Gly	Pro	Gly	Gln	Lys	Gly	Leu	Cys	Ser					
				890					895					900					
Pro	Arg	Pro	Asn	Ile	Leu	His	Leu	Asp	Val	Asp	Ser	Arg	Asp	Arg					
				905					910					915					
Arg	Arg	Arg	Glu	Leu	Glu	Pro	Pro	Glu	Gln	Gln	Glu	Pro	Gly	Glu					
				920					925					930					
Arg	Gln	Glu	Pro	Ser	Met	Ser	Trp	Trp	Pro	Val	Ser	Ser	Ala	Glu					
				935					940					945					
Lys	Lys	Lys	Asn	Ile	Thr	Leu	Asp	Cys	Ala	Arg	Gly	Thr	Ala	Asn					
				950					955					960					

Cys	Val	Val	Phe	Ser	Cys	Pro	Leu	Tyr	Ser	Phe	Asp	Arg	Ala	Ala	
				965					970					975	
Val	Leu	His	Val	Trp	Gly	Arg	Leu	Trp	Asn	Ser	Thr	Phe	Leu	Glu	
				980					985					990	
Glu	Tyr	Ser	Ala	Val	Lys	Ser	Leu	Glu	Val	Ile	Val	Arg	Ala	Asn	
				995					1000					1005	
Ile	Thr	Val	Lys	Ser	Ser	Ile	Lys	Asn	Leu	Met	Leu	Arg	Asp	Ala	
				1010					1015					1020	
Ser	Thr	Val	Ile	Pro	Val	Met	Val	Tyr	Leu	Asp	Pro	Met	Ala	Val	
				1025					1030					1035	
Val	Ala	Glu	Gly	Val	Pro	Trp	Trp	Val	Ile	Leu	Leu	Ala	Val	Leu	
				1040					1045					1050	
Ala	Gly	Leu	Leu	Val	Leu	Ala	Leu	Leu	Val	Leu	Leu	Leu	Trp	Lys	
				1055					1060					1065	
Met	Gly	Phe	Phe	Lys	Arg	Ala	Lys	His	Pro	Glu	Ala	Thr	Val	Pro	
				1070					1075					1080	
Gln	Tyr	His	Ala	Val	Lys	Ile	Pro	Arg	Glu	Asp	Arg	Gln	Gln	Phe	
				1085					1090					1095	
Lys	Glu	Glu	Lys	Thr	Gly	Thr	Ile	Leu	Arg	Asn	Asn	Trp	Gly	Ser	
				1100					1105					1110	
Pro	Arg	Arg	Glu	Gly	Pro	Asp	Ala	His	Pro	Ile	Leu	Ala	Ala	Asp	
				1115					1120					1125	
Gly	His	Pro	Glu	Leu	Gly	Pro	Asp	Gly	His	Pro	Gly	Pro	Gly	Thr	
				1130					1135					1140	
Ala															

<210> 438
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 438
 ggctgacacc gcagtgtctt tcag 24

<210> 439
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 439
gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

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ggagctgcga gcacagtgtt ggctcacaac aagatgtctc aggtgtcagc 150
cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctcgcagctg 200
ccgcggcggg ggctgcagcc ggggggcggg cggacggcgg taattttctg 250
gatgataaac aatgggtcac cacaatctct cagtatgaca aggaagtcgg 300
acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350
ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400
tgcttaaaga tgaaatgtag tcgccataaa gtatgcattg ctcaagattc 450
tcagactgca gtctgcatta gtcaccggag gcttacacac aggatgaaag 500
aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550
aagcagtgcc cagtgggtcta tcccagccct gtttgtgggt cagatggtca 600
tacctactct tttcagtgc aactagaata tcaggcatgt gtcttaggaa 650
aacagatctc agtcaaagt gaaggacatt gcccatgtcc ttcagataag 700
cccaccagta caagcagaaa tgtaagaga gcatgcagt acctggagtt 750
caggggaagt gcaaacagat tgcgggactg gttcaaggcc cttcatgaaa 800
gtggaagtca aaacaagaag acaaaaacat tgctgaggcc tgagagaagc 850
agattcgata ccagcatctt gccaatgtgc aaggactcac ttggctggat 900
gtttaacaga cttgatacaa actatgacct gctattggac cagtcaagc 950

tcagaagcat ttaccttgat aagaatgaac agtgtaccaa ggcattcttc 1000
aattcttgtg acacatacaa ggacagttta atatctaata atgagtgggtg 1050
ctactgcttc cagagacagc aagacccacc ttgccagact gagctcagca 1100
atattcagaa gcggcaaggg gtaaagaagc toctaggaca gtatatcccc 1150
ctgtgtgatg aagatgggta ctacaagcca acacaatgtc atggcagtgt 1200
tggacagtgc tgggtgtgtg acagatatgg aatgaagtc atgggatcca 1250
gaataaatgg tgttcagat tgtgctatag attttgagat ctccggagat 1300
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cgatattatg aatgatgaag atgaaattga agatgatgat gaagatgaag 1400
gggatgatga tgatgggtgt gatgaccatg atgtatacat ttgattgatg 1450
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ctactataat aaatttttca cgagaacaaa ctttgtaa atctccataag 1750
caaatgaca gctagtgtt gggatcgta atgttaattt tttgaaagat 1800
aattctaagt gaaattttaa ataaataaat ttttaatgac ctgggtctta 1850
aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900
ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950
aaaaaaaaaaaa 1964

<210> 442

<211> 436

<212> PRT

<213> Homo sapiens

<400> 442

Met	Leu	Lys	Val	Ser	Ala	Val	Leu	Cys	Val	Cys	Ala	Ala	Ala	Trp
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Cys	Ser	Gln	Ser	Leu	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ala	Ala	Gly
				20					25					30

Gly	Arg	Ser	Asp	Gly	Gly	Asn	Phe	Leu	Asp	Asp	Lys	Gln	Trp	Leu
				35					40					45

Thr	Thr	Ile	Ser	Gln	Tyr	Asp	Lys	Glu	Val	Gly	Gln	Trp	Asn	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50										55					60				
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro					
				65					70					75					
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys					
				80					85					90					
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp					
				95					100					105					
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg					
				110					115					120					
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile					
				125					130					135					
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val					
				140					145					150					
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu					
				155					160					165					
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu					
				170					175					180					
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg					
				185					190					195					
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala					
				200					205					210					
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser					
				215					220					225					
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg					
				230					235					240					
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp					
				245					250					255					
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln					
				260					265					270					
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr					
				275					280					285					
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile					
				290					295					300					
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro					
				305					310					315					
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val					
				320					325					330					
Lys	Lys	Leu	Leu	Gly	Gln	Tyr	Ile	Pro	Leu	Cys	Asp	Glu	Asp	Gly					
				335					340					345					

Tyr	Tyr	Lys	Pro	Thr	Gln	Cys	His	Gly	Ser	Val	Gly	Gln	Cys	Trp
				350					355					360
Cys	Val	Asp	Arg	Tyr	Gly	Asn	Glu	Val	Met	Gly	Ser	Arg	Ile	Asn
				365					370					375
Gly	Val	Ala	Asp	Cys	Ala	Ile	Asp	Phe	Glu	Ile	Ser	Gly	Asp	Phe
				380					385					390
Ala	Ser	Gly	Asp	Phe	His	Glu	Trp	Thr	Asp	Asp	Glu	Asp	Asp	Glu
				395					400					405
Asp	Asp	Ile	Met	Asn	Asp	Glu	Asp	Glu	Ile	Glu	Asp	Asp	Asp	Glu
				410					415					420
Asp	Glu	Gly	Asp	Asp	Asp	Asp	Gly	Gly	Asp	Asp	His	Asp	Val	Tyr
				425					430					435

Ile

<210> 443
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 443
 cagcaatatt cagaagcggc aaggg 25

<210> 444
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 444
 catcatggtc atcaccacca tcatcatc 28

<210> 445
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 445
 gggtactaca agccaacaca atgtcatggc agtggttgac agtgctgg 48

<210> 446
 <211> 3617
 <212> DNA
 <213> Homo sapiens

<400> 446

cagactccag atttccctgt caaccacgag gagtccagag aggaaacgcg 50
gagcggagac aacagtacct gacgcctctt tcagcccggg atcgccccag 100
cagggatggg cgacaagatc tggctgccct tccccgtgct ccttctggcc 150
gctctgcctc cggtgctgct gcctggggcg gcoggettca caccttcctt 200
cgatagcgac ttcaccttta cccttccgcg cggccagaag gaggcttctt 250
accagcccat gccctgaag gcctcgctgg agatcgagta ccaagtttta 300
gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350
aaccttagtt tttgaacaaa gaaaatcaga tggagttcac actgtagaga 400
ctgaagtggg tgattacatg ttctgctttg acaatacatt cagcaccatt 450
tctgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500
ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550
tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600
agactaagca aaagtgggca catacaaatt ctgcttagag catttgaagc 650
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ctatggttaa tttagtggtc atggtggtgg tgtcagccat tcaagtttat 750
atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaactc 800
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gagtattggg cctaattgca acaccagtct gtttttaaca ggttctatta 1150
cccagaactt ttttgtaa at gcggcagtta caaattaact gtggaagttt 1200
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tagtctttgt actttgctta cattcccaaa agctgacatt ttcacgattc 1450

ttaaaaacac aaagttacac ttactaaaat taggacatgt tttctctttg 1500
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 gtagaactat aaataaatat ctagaatctg actggctcat catgacatcc 1900
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 atttaactaa ggcccaaccg atttccataa tgtagcagtt accgtgttca 3250
 cctcacacta aggcctagag tttgctctga tatgcatttg gatgattaat 3300
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 gtgaaatttt aaaagacatt gattccgcat gtaaggattt ttcacttgaa 3500
 gtacaataat gcacaatcag tggtgctcaa actgctttat acttataaac 3550
 agccatotta aataagcaac gtattgtgag tactgatatg tatataataa 3600
 aaattatcaa agaaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

Met	Gly	Asp	Lys	Ile	Trp	Leu	Pro	Phe	Pro	Val	Leu	Leu	Leu	Ala
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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30
Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45
Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60
Glu	Tyr	Gln	Val	Leu	Asp	Gly	Ala	Gly	Leu	Asp	Ile	Asp	Phe	His
				65					70					75
Leu	Ala	Ser	Pro	Glu	Gly	Lys	Thr	Leu	Val	Phe	Glu	Gln	Arg	Lys
				80					85					90
Ser	Asp	Gly	Val	His	Thr	Val	Glu	Thr	Glu	Val	Gly	Asp	Tyr	Met
				95					100					105
Phe	Cys	Phe	Asp	Asn	Thr	Phe	Ser	Thr	Ile	Ser	Glu	Lys	Val	Ile

<210> 451
 <211> 859
 <212> DNA
 <213> Homo sapiens

<400> 451
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 agcataccag atctcaccag agagtcgcag acactatgct gcctcccatg 100
 gccctgcccga gtgtgtcctg gatgctgctt tcctgcctca ttctcctgtg 150
 tcaggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200
 gctgtcccaa aggtccaag gcctatggct cccctgcta tgccttggtt 250
 ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300
 ctctggaaaa ctggtgtctg tgctcagtgg ggctgagggga tccttcgtgt 350
 cctccctggg gaggagcatt agtaacagct actcatacat ctggattggg 400
 ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450
 gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500
 ccatcttaaa ccctggccac tgtgggagcc tgtcaagaag cacaggattt 550
 ctgaagtgga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600
 gttcaaggac tagggcagggt gggaagtcag cagcctcagc ttggcgtgca 650
 gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700
 ttctcccaaa actgccctac ctgactacct tgtcatgac ctccttcttt 750
 ttcttttttc ttcaccttca tttcaggctt ttctctgtct tccatgtctt 800
 gagatctcag agaataataa taaaaatgtt actttataaa aaaaaaaaaa 850
 aaaaaaaaaa 859

<210> 452
 <211> 175
 <212> PRT
 <213> Homo sapiens

<400> 452
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 Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln
 20 25 30
 Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys
 35 40 45
 Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser

	50		55		60
Trp Met Asp Ala Asp	Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys				
	65		70		75
Leu Val Ser Val Leu	Ser Gly Ala Glu Gly Ser Phe Val Ser Ser				
	80		85		90
Leu Val Arg Ser Ile	Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly				
	95		100		105
Leu His Asp Pro Thr	Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp				
	110		115		120
Glu Trp Ser Ser Thr	Asp Val Met Asn Tyr Phe Ala Trp Glu Lys				
	125		130		135
Asn Pro Ser Thr Ile	Leu Asn Pro Gly His Cys Gly Ser Leu Ser				
	140		145		150
Arg Ser Thr Gly Phe	Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala				
	155		160		165
Lys Leu Pro Tyr Val	Cys Lys Phe Lys Asp				
	170		175		

<210> 453
 <211> 550
 <212> DNA
 <213> Homo sapiens

<400> 453
 ccagtctgtc gccacctcac ttggtgtctg ctgtccccgc caggcaagcc 50
 tgggggtgaga gcacagagga gtgggcccgg accatgcggg ggacgcggct 100
 ggcgctcctg gcgctggtgc tggctgcctg cggagagctg gcgcgggccc 150
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 Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser
 65 70 75
 Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro
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 Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro
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<211> 1518

<212> DNA

<213> Homo sapiens

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<211> 266

<212> PRT

<213> Homo sapiens

<400> 456

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Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu
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Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys
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Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly
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Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser
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<212> DNA

<213> Homo sapiens

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Leu	Ala	His	His	Arg 320	Trp	Leu	Leu	Phe	Phe 325	His	Phe	Gly	Lys	Asn 330
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Lys	Asn	Asp	His	Ile 350	Gln	Val	Gly	Arg	Phe 355	Asp	Cys	Ser	Ser	Ala 360
Pro	Asp	Ile	Cys	Ser 365	Asn	Leu	Tyr	Val	Phe 370	Gln	Pro	Ser	Leu	Ala 375
Val	Phe	Lys	Gly	Gln 380	Gly	Thr	Lys	Glu	Tyr 385	Glu	Ile	His	His	Gly 390
Lys	Lys	Ile	Leu	Tyr 395	Asp	Ile	Leu	Ala	Phe 400	Ala	Lys	Glu	Ser	Val 405
Asn	Ser	His	Val	Thr 410	Thr	Leu	Gly	Pro	Gln 415	Asn	Phe	Pro	Ala	Asn 420
Asp	Lys	Glu	Pro	Trp 425	Leu	Val	Asp	Phe	Phe 430	Ala	Pro	Trp	Cys	Pro 435
Pro	Cys	Arg	Ala	Leu 440	Leu	Pro	Glu	Leu	Arg 445	Arg	Ala	Ser	Asn	Leu 450
Leu	Tyr	Gly	Gln	Leu 455	Lys	Phe	Gly	Thr	Leu 460	Asp	Cys	Thr	Val	His 465
Glu	Gly	Leu	Cys	Asn 470	Met	Tyr	Asn	Ile	Gln 475	Ala	Tyr	Pro	Thr	Thr 480
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 461
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<210> 462
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 462
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<210> 463
<211> 1818
<212> DNA
<213> Homo sapiens

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 <211> 300
 <212> PRT
 <213> Homo sapiens

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His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln		50	55	60
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu		65	70	75
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr		80	85	90
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Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly		155	160	165
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Tyr	Leu	Ile	Pro	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	Val	Gly	Phe		185	190	195
His	Arg	Gly	Leu	Thr	Ser	Glu	Leu	Gln	Ala	Leu	Gly	Lys	Thr	Gly		200	205	210
Ile	Lys	Thr	Ser	Cys	Leu	Cys	Pro	Val	Phe	Val	Asn	Thr	Gly	Phe		215	220	225
Thr	Lys	Asn	Pro	Ser	Thr	Arg	Leu	Trp	Pro	Val	Leu	Glu	Thr	Asp		230	235	240
Glu	Val	Val	Arg	Ser	Leu	Ile	Asp	Gly	Ile	Leu	Thr	Asn	Lys	Lys		245	250	255
Met	Ile	Phe	Val	Pro	Ser	Tyr	Ile	Asn	Ile	Phe	Leu	Arg	Leu	Gln		260	265	270
Lys	Phe	Leu	Pro	Glu	Arg	Ala	Ser	Ala	Ile	Leu	Asn	Arg	Met	Gln		275	280	285
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<211> 1547

<212> DNA

<213> Homo sapiens

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 gctgtggctg gtgctggggg cgggtgtcat gatcctgctg atcatcgtgt 200
 actgggacag cgcaggcgcc gcgcacttct acttgcacac gtcctttctct 250
 aggccgcaca cggggccgcc gctgcccacg cccgggcccg acagggacag 300
 ggagctcacg gccgactccg atgtcgacga gtttctggac aagttttctca 350
 gtgctggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccg 400
 cctgcgccgg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450
 gcgcgacgcc cggcgcagcc cagaccaggg ccggcagcag gcggagcgga 500
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 aaggagcgcg cattcgacga catccccaac tcggagctga gccacctgat 600
 cgtggacgac cggcacgggg ccatctactg ctacgtgccc aaggtggcct 650
 gcaccaactg gaagcgcgtg atgatcgtgc tgagcggaag cctgctgcac 700
 cgcggtgcmc cctaccgcga cccgctgcmc atcccgcmc agcacgtgca 750
 caacgccagc gcgcacctga ctttcaacaa gttctggcmc cgctacggga 800
 agctctcccg ccacctcatg aaggtcaagc tcaagaagta caccaagttc 850
 ctcttcgtgc gcgaccctt cgtgcgcctg atctccgcct tccgcagcaa 900
 gttcgagctg gagaacgagg agttctaccg caagttcgcc gtgcccattgc 950
 tgccgctgta cgccaaccac accagcctgc ccgcctcggc gcgcgaggcc 1000
 ttccgcgctg gcctcaaggt gtccttcgcc aacttcatcc agtacctgct 1050
 ggaccgcac acggagaagc tggcgccctt caacgagcac tggcggcagg 1100
 tgtaccgcct ctgccacccg tgccagatcg actacgactt cgtggggaag 1150
 ctggagactc tggacgagga cgccgcgag ctgctgcagc tactccaggt 1200
 ggaccggcag ctccgcttcc ccccgagcta ccggaacagg accgccagca 1250
 gctgggagga ggactggttc gccaaatcc ccctggcctg gaggcagcag 1300
 ctgtataaac tctacgaggc cgactttgtt ctcttcggct accccaagcc 1350
 cgaaaacctc ctccgagact gaaagcttcc gcgttgcttt ttctcgcgtg 1400
 cctggaacct gacgcacgcg cactccagtt tttttatgac ctacgatttt 1450

gcaatctggg cttcttggtc actccactgc ctctatccat tgagtactgt 1500

atcgatatgg ttttttaaga ttaatatatt tcaggtatatt aatacga 1547

<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met Thr Lys Ala Arg Leu Phe Arg Leu Trp Leu Val Leu Gly Ser
1 5 10 15

Val Phe Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly
20 25 30

Ala Ala His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr
35 40 45

Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu
50 55 60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser
65 70 75

Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln
80 85 90

Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp
95 100 105

Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln
110 115 120

Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser
125 130 135

Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro
140 145 150

Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala
155 160 165

Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg
170 175 180

Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro
185 190 195

Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala
200 205 210

Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys
215 220 225

Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys
230 235 240

00076188-1054

Phe Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe
245 250 255

Arg Ser Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe
260 265 270

Ala Val Pro Met Leu Arg Leu Tyr Ala Asn His Thr Ser Leu Pro
275 280 285

Ala Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys Val Ser Phe
290 295 300

Ala Asn Phe Ile Gln Tyr Leu Leu Asp Pro His Thr Glu Lys Leu
305 310 315

Ala Pro Phe Asn Glu His Trp Arg Gln Val Tyr Arg Leu Cys His
320 325 330

Pro Cys Gln Ile Asp Tyr Asp Phe Val Gly Lys Leu Glu Thr Leu
335 340 345

Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg
350 355 360

Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser
365 370 375

Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln
380 385 390

Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr
395 400 405

Pro Lys Pro Glu Asn Leu Leu Arg Asp
410

<210> 467
<211> 1071
<212> DNA
<213> Homo sapiens

<400> 467
tcgggccaga attcggcacg aggcggcacg agggcgacgg cctcacgggg 50
ctttggaggt gaaagaggcc cagagtagag agagagagag accgacgtac 100
acgggatggc tacgggaacg cgctatgccg ggaaggtggt ggtcgtgacc 150
gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200
cggggcccga gtggttatct gcgacaagga tgagtctggg ggccggggccc 250
tgagacagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300
gaagatgatg tgaagacctt gggttctgag accatccgcc gatttggccg 350
cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400

ctgaggagac ctctgccag ggattccgcc agctgctgga gctgaaccta 450
ctggggacgt acaccttgac caagctcgcc ctcccctacc tgcggaagag 500
tcaagggaat gtcataca tctccagcct ggtgggggca atcggccagg 550
cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600
aaagctttgg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650
ctccccagga aacatctgga ccccgctgtg ggaggagctg gcagccttaa 700
tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750
ggccgcatgg gccagcccgc tgaggtcggg gctgcggcag tgttcctggc 800
ctccgaagcc aacttctgca cgggcattga actgctcgtg acgggggggtg 850
cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900
cccgatatcc ctctctgatt tctctcattt ctacttgggg ccccttcct 950
aggactctcc caccctaaac tccaacctgt atcagatgca gcccctaac 1000
ccttagactc taagcccagt tagcaagggtg ccgggtcacc ctgcaggttc 1050
ccataaaaac gatttgcagc c 1071

<210> 468
<211> 270
<212> PRT
<213> Homo sapiens

<400> 468
Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr
1 5 10 15
Gly Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val
20 25 30
Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly
35 40 45
Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu
50 55 60
Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu
65 70 75
Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala
80 85 90
Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln
95 100 105
Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr
110 115 120

Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn	125	130	135
Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln	140	145	150
Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr	155	160	165
Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn	170	175	180
Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu	185	190	195
Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met	200	205	210
Leu Ala Gln Pro Leu Gly Arg Met Gly Gln Pro Ala Glu Val Gly	215	220	225
Ala Ala Ala Val Phe Leu Ala Ser Glu Ala Asn Phe Cys Thr Gly	230	235	240
Ile Glu Leu Leu Val Thr Gly Gly Ala Glu Leu Gly Tyr Gly Cys	245	250	255
Lys Ala Ser Arg Ser Thr Pro Val Asp Ala Pro Asp Ile Pro Ser	260	265	270

<210> 469
 <211> 687
 <212> DNA
 <213> Homo sapiens

<400> 469
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 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100
 ccagcccagg agccccaaaa gcaagaggaa ggggcaagg cggcctgggc 150
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgaggtca 300
 acttgcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400
 gtgccttgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450
 gcatggtgag cgtgccggtg ttcagccagg ttctgtgctg ccgccgcctc 500
 tgcccgccac cgccccgcac agggccttgc cgccagcgcg cagtcattgga 550

gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600
gccaggccag cagcccagaga ccatactcct tgcacctttg tgccaagaaa 650
ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470
<211> 180
<212> PRT
<213> Homo sapiens

<400> 470
Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile
1 5 10 15
Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
20 25 30
Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val
35 40 45
Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu
50 55 60
Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn
65 70 75
Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu
80 85 90
Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile
95 100 105
Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg
110 115 120
Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp
125 130 135
Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
140 145 150
Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln
155 160 165
Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
170 175 180

<210> 471
<211> 2368
<212> DNA
<213> Homo sapiens

<400> 471
gcgcccag gcgtaggcgg ggtggccctt gcgtctcccg cttccttgaa 50
aaaccgcgag ggcgagcgag gctgcgggcc ggccgctgcc cttccccaca 100

cctgagcatc cccaaagtgt aacgtagaag ccttgcatcc ttttcttggtg 1600
 taaagtatatt atttttgtca aattgcagga aacatcagga accacagtgc 1650
 atgaaaaatc tttcacagct agaaattgaa agggccttgg gtatagagag 1700
 cagctcagaa gtcattcccag ccctctgaat ctctgtgtgt atgtttttatt 1750
 tcttaccttt aattttttcca gcattttccac catgggcatt caggctctcc 1800
 acactcttca ctattatctc ttgggtcagag gactccaata acagccaggt 1850
 ttacatgaac tgtgtttgtt cattctgacc taaggggttt agataatcag 1900
 taaccataac ccctgaagct gtgactgcca aacatctcaa atgaaatgtt 1950
 gtggccatca gagactcaaa aggaagtaag gatttttaca gacagattaa 2000
 aaaaaaattg ttttgtccaa aatatagttg ttgttgattt ttttttaagt 2050
 tttctaagca atattttttca agccagaagt cctctaagtc ttgccagtac 2100
 aaggtagtct tgtgaagaaa agttgaatac tgttttgattt tcatctcaag 2150
 gggttccctg ggtcttgaac tactttaata ataactaaaa aaccacttct 2200
 gattttcctt cagtgatgtg cttttggtga aagaattaat gaactccagt 2250
 acctgaaagt gaaagatttg attttgtttc catcttctgt aatcttccaa 2300
 agaattatat ctttgtaaatt ctctcaatac tcaatctact gtaagtaccc 2350
 agggaggcta atttcttt 2368

<210> 472
 <211> 349
 <212> PRT
 <213> Homo sapiens

<400> 472
 Met Ala Gly Gly Arg Cys Gly Pro Gln Leu Thr Ala Leu Leu Ala
 1 5 10 15
 Ala Trp Ile Ala Ala Val Ala Ala Thr Ala Gly Pro Glu Glu Ala
 20 25 30
 Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser
 35 40 45
 Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr
 50 55 60
 Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu
 65 70 75
 Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys
 80 85 90

Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val	95	100	105
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg	110	115	120
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile	125	130	135
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys	140	145	150
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser	155	160	165
Ile	Ser	Gly	Lys	Ile	Trp	His	Leu	His	Asn	Tyr	Phe	Thr	Val	Thr	170	175	180
Leu	Gly	Ile	Pro	Ala	Trp	Cys	Ser	Tyr	Val	Phe	Phe	Val	Ile	Ala	185	190	195
Thr	Leu	Val	Phe	Gly	Leu	Phe	Met	Gly	Leu	Val	Leu	Val	Val	Ile	200	205	210
Ser	Glu	Cys	Phe	Tyr	Val	Pro	Leu	Pro	Arg	His	Leu	Ser	Glu	Arg	215	220	225
Ser	Glu	Gln	Asn	Arg	Arg	Ser	Glu	Glu	Ala	His	Arg	Ala	Glu	Gln	230	235	240
Leu	Gln	Asp	Ala	Glu	Glu	Glu	Lys	Asp	Asp	Ser	Asn	Glu	Glu	Glu	245	250	255
Asn	Lys	Asp	Ser	Leu	Val	Asp	Asp	Glu	Glu	Glu	Lys	Glu	Asp	Leu	260	265	270
Gly	Asp	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asn	Leu	275	280	285
Ala	Ala	Gly	Val	Asp	Glu	Glu	Arg	Ser	Glu	Ala	Asn	Asp	Gln	Gly	290	295	300
Pro	Pro	Gly	Glu	Asp	Gly	Val	Thr	Arg	Glu	Glu	Val	Glu	Pro	Glu	305	310	315
Glu	Ala	Glu	Glu	Gly	Ile	Ser	Glu	Gln	Pro	Cys	Pro	Ala	Asp	Thr	320	325	330
Glu	Val	Val	Glu	Asp	Ser	Leu	Arg	Gln	Arg	Lys	Ser	Gln	His	Ala	335	340	345

Asp Lys Gly Leu

<210> 473
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 473
gtccagccca tgaccgcctc caac 24

<210> 474
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 474
ctctcctcat ccacaccagc agcc 24

<210> 475
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 475
gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476
<211> 2478
<212> DNA
<213> Homo sapiens

<400> 476
atctggttga actacttaag cttaatttgt taaactccgg taagtaccta 50
gcccatga ttgactcag agattctctt ttgtccacag acagtcattc 100
caggggcaga aagaaaagag ctcccaaagt ctatatctat tcaggggctc 150
tcaagaacaa tggaatatca tcctgattta gaaaatttgg atgaagatgg 200
atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250
tttcagagaa aggatcgtgt gctgcatctc ctcttgggc cctcattgct 300
gtaatttttg gaatcctatg cttggtaata ctggtgatag ctgtggtcct 350
gggtaccatg ggggttcttt ccagcccttg tcctcctaatt tggattatat 400
atgagaagag ctgttatcta ttcagcatgt cactaaattc ctgggatgga 450
agtaaaagac aatgctggca actgggctct aatctcctaa agatagacag 500
ctcaaataaa ttgggattta tagtaaaaca agtgtcttcc caacctgata 550
attcattttg gataggcctt tctcggtccc agactgaggt accatggctc 600

tgggaggatg gatcaacatt ctcttctaac ttatttcaga tcagaaccac 650
 agctacccaa gaaaacccat ctccaaattg tgtatggatt cacgtgtcag 700
 tcatttatga ccaactgtgt agtgtgccct catatagtat ttgtgagaag 750
 aagttttcaa tgtaagagga aggggtggaga aggagagaga aatatgtgag 800
 gtagtaagga ggacagaaaa cagaacagaa aagagtaaca gctgaggtca 850
 agataaatgc agaaaatggt tagagagctt ggccaactgt aatcttaacc 900
 aagaaattga agggagaggc tgtgatttct gtatttgtcg acctacaggt 950
 aggctagtat tatttttcta gttagtagat ccctagacat ggaatcaggg 1000
 cagccaagct tgagttttta ttttttattt atttattttt ttgagatagg 1050
 gtctcacttt gttaccacag ctggagtgc gtggcacaat ctcgactcac 1100
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 gccatgttga ccaagctggt ctctaactcc tgggcttaag tgatctgccc 1250
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 gcccacagct tgaattttca ttctgccatt gacttggcat ttaccttggg 1350
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 tcaacaatgc cattgaagtg cacggtgtgt tgccacgatt tgacctcaa 1450
 cttctagcag tatatcagtt atgaactgag ggtgaaatat atttctgaat 1500
 agctaaatga agaaatggga aaaaatcttc accacagtca gagcaatttt 1550
 attattttca tcagtatgat cataattatg attatcatct tagtaaaaag 1600
 caggaaactcc tactttttct ttatcaatta aatagctcag agagtacatc 1650
 tgccatatct ctaatagaat cttttttttt tttttttttt ttgagacag 1700
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 acaggcgtga gccactgcac ccagcctaga atcttgtata atatgtaatt 2000
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tacataaaaa tacataaaat ctgatgatga atataaaaaa gtaaccaacc 2100
tcattggaac aagtattaac attttggaat atgttttatt agttttgtga 2150
tgtactgttt tacaattttt accatttttt tcagtaatta ctgtaaaatg 2200
gtattattgg aatgaaacta tatttcctca tgtgctgatt tgtcttattt 2250
ttttcatact ttcccactgg tgctattttt atttccaatg gatattttctg 2300
tattactagg gaggcattta cagtcctcta atgttgatta atatgtgaaa 2350
agaaattgta ccaattttac taaattatgc agttttaaag ggatgatttt 2400
atgttatgtg gatttcattt caataaaaaa aaactcttat caaaaaaaaaa 2450
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2478

<210> 477

<211> 201

<212> PRT

<213> Homo sapiens

<400> 477

Met	Glu	Tyr	His	Pro	Asp	Leu	Glu	Asn	Leu	Asp	Glu	Asp	Gly	Tyr	1	5	10	15
Thr	Gln	Leu	His	Phe	Asp	Ser	Gln	Ser	Asn	Thr	Arg	Ile	Ala	Val	20	25	30	
Val	Ser	Glu	Lys	Gly	Ser	Cys	Ala	Ala	Ser	Pro	Pro	Trp	Arg	Leu	35	40	45	
Ile	Ala	Val	Ile	Leu	Gly	Ile	Leu	Cys	Leu	Val	Ile	Leu	Val	Ile	50	55	60	
Ala	Val	Val	Leu	Gly	Thr	Met	Gly	Val	Leu	Ser	Ser	Pro	Cys	Pro	65	70	75	
Pro	Asn	Trp	Ile	Ile	Tyr	Glu	Lys	Ser	Cys	Tyr	Leu	Phe	Ser	Met	80	85	90	
Ser	Leu	Asn	Ser	Trp	Asp	Gly	Ser	Lys	Arg	Gln	Cys	Trp	Gln	Leu	95	100	105	
Gly	Ser	Asn	Leu	Leu	Lys	Ile	Asp	Ser	Ser	Asn	Glu	Leu	Gly	Phe	110	115	120	
Ile	Val	Lys	Gln	Val	Ser	Ser	Gln	Pro	Asp	Asn	Ser	Phe	Trp	Ile	125	130	135	
Gly	Leu	Ser	Arg	Pro	Gln	Thr	Glu	Val	Pro	Trp	Leu	Trp	Glu	Asp	140	145	150	
Gly	Ser	Thr	Phe	Ser	Ser	Asn	Leu	Phe	Gln	Ile	Arg	Thr	Thr	Ala	155	160	165	
Thr	Gln	Glu	Asn	Pro	Ser	Pro	Asn	Cys	Val	Trp	Ile	His	Val	Ser				

<400> 482

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 tcttgggtca tcgtaacctc cacctcccgg gttcaagtga ttctcatgcc 150
 tcagcctccc gagtagctgg gattacagggt ggtgacttcc aagagtgact 200
 ccgtcggagg aaaatgactc ccagtcgct gctgcagacg aactgttcc 250
 tgctgagtct gctcttcctg gtccaagggtg cccacggcag gggccacagg 300
 gaagactttc gcttctgcag ccagcggaac cagacacaca ggagcagcct 350
 ccactacaaa cccacaccag acctgcgcat ctccatcgag aactccgaag 400
 aggccctcac agtccatgcc cctttccctg cagcccaccc tgcttcccga 450
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 aaaagggacc tccagctgct cagccagttc ctgaagcatc cccagaaggc 800
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn
 50 55 60
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His
 65 70 75

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Thr	Ile	Ala	Ala	Tyr 425	Leu	Cys	Ser	Arg	Val 430	Pro	Leu	Pro	Cys	Arg 435
Arg	Lys	Pro	Arg	Asp 440	Tyr	Thr	Ile	Lys	Val 445	His	Met	Asn	Leu	Leu 450
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Val	Ala	Leu	Thr	Gly 470	Ser	Glu	Ala	Gly	Cys 475	Arg	Ala	Ser	Ala	Ile 480
Phe	Leu	His	Phe	Ser 485	Leu	Leu	Thr	Cys	Leu 490	Ser	Trp	Met	Gly	Leu 495
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Val	Ile	Tyr	Pro	Ser 560	Met	Cys	Trp	Ile	Arg 565	Asp	Ser	Leu	Val	Ser 570
Tyr	Ile	Thr	Asn	Leu 575	Gly	Leu	Phe	Ser	Leu 580	Val	Phe	Leu	Phe	Asn 585
Met	Ala	Met	Leu	Ala 590	Thr	Met	Val	Val	Gln 595	Ile	Leu	Arg	Leu	Arg 600
Pro	His	Thr	Gln	Lys 605	Trp	Ser	His	Val	Leu 610	Thr	Leu	Leu	Gly	Leu 615
Ser	Leu	Val	Leu	Gly 620	Leu	Pro	Trp	Ala	Leu 625	Ile	Phe	Phe	Ser	Phe 630
Ala	Ser	Gly	Thr	Phe 635	Gln	Leu	Val	Val	Leu 640	Tyr	Leu	Phe	Ser	Ile 645
Ile	Thr	Ser	Phe	Gln 650	Gly	Phe	Leu	Ile	Phe 655	Ile	Trp	Tyr	Trp	Ser 660

21

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680 685 690

Ser Arg Ile

<210> 484
<211> 516
<212> DNA
<213> Homo sapiens

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<222> 68, 70, 84, 147
<223> unknown base

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 487
<211> 2849
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2715
<223> unknown base

<400> 487
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gcgattctct gctgccagag caggctcggc gcttcacccc cagtgcagcc 200
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cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450
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<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

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Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln	
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His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser	
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Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp	
				65					70					75	
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe	
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Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys	
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Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu	
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Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser	
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Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe	
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Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro	
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Gln	Phe	Thr	Glu	Ala	Val	Ser	Pro	Ser	Val	Leu	Pro	Pro	Ser	Ala	
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<223> Synthetic oligonucleotide probe

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<210> 492

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 492

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<210> 493

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 493

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<210> 494

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

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Ala	Pro	Cys	Lys	Asn	Asn	Ser	Pro	Leu	Gln	Ile	Pro	Val	Asn	Ala	
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Phe	Asp	Ala	Leu	Thr	Glu	Leu	Lys	Val	Leu	Arg	Leu	His	Ser	Asn	
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Leu	Gln	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Phe	Leu	Ala	Lys	Glu	Ile	
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Gly	Asp	Ala	Lys	Phe	Leu	His	Phe	Leu	Pro	Ser	Leu	Ile	Gln	Leu	
				335					340					345	
Asp	Leu	Ser	Phe	Asn	Phe	Glu	Leu	Gln	Val	Tyr	Arg	Ala	Ser	Met	
				350					355					360	
Asn	Leu	Ser	Gln	Ala	Phe	Ser	Ser	Leu	Lys	Ser	Leu	Lys	Ile	Leu	
				365					370					375	
Arg	Ile	Arg	Gly	Tyr	Val	Phe	Lys	Glu	Leu	Lys	Ser	Phe	Asn	Leu	
				380					385					390	
Ser	Pro	Leu	His	Asn	Leu	Gln	Asn	Leu	Glu	Val	Leu	Asp	Leu	Gly	
				395					400					405	
Thr	Asn	Phe	Ile	Lys	Ile	Ala	Asn	Leu	Ser	Met	Phe	Lys	Gln	Phe	
				410					415					420	
Lys	Arg	Leu	Lys	Val	Ile	Asp	Leu	Ser	Val	Asn	Lys	Ile	Ser	Pro	
				425					430					435	
Ser	Gly	Asp	Ser	Ser	Glu	Val	Gly	Phe	Cys	Ser	Asn	Ala	Arg	Thr	
				440					445					450	
Ser	Val	Glu	Ser	Tyr	Glu	Pro	Gln	Val	Leu	Glu	Gln	Leu	His	Tyr	
				455					460					465	
Phe	Arg	Tyr	Asp	Lys	Tyr	Ala	Arg	Ser	Cys	Arg	Phe	Lys	Asn	Lys	
				470					475					480	
Glu	Ala	Ser	Phe	Met	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	
				485					490					495	
Gln	Thr	Leu	Asp	Leu	Ser	Lys	Asn	Ser	Ile	Phe	Phe	Val	Lys	Ser	
				500					505					510	
Ser	Asp	Phe	Gln	His	Leu	Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	
				515					520					525	
Gly	Asn	Leu	Ile	Ser	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	
				530					535					540	
Leu	Ala	Glu	Leu	Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp	

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Leu Leu His Ser Thr Ala Phe Glu Glu	Leu His Lys Leu Glu Val	
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Leu Asp Ile Ser Ser Asn Ser His Tyr	Phe Gln Ser Glu Gly Ile	
575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn	Leu Lys Val Leu Gln Lys	
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Leu Met Met Asn Asp Asn Asp Ile Ser	Ser Ser Thr Ser Arg Thr	
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Met Glu Ser Glu Ser Leu Arg Thr Leu	Glu Phe Arg Gly Asn His	
620	625	630
Leu Asp Val Leu Trp Arg Glu Gly Asp	Asn Arg Tyr Leu Gln Leu	
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Phe Lys Asn Leu Leu Lys Leu Glu Glu	Leu Asp Ile Ser Lys Asn	
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Ser Leu Ser Phe Leu Pro Ser Gly Val	Phe Asp Gly Met Pro Pro	
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680	685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys	Asn Leu Glu Thr Leu Asp	
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Cys Ser Arg Ser Leu Lys Asn Leu Ile	Leu Lys Asn Asn Gln Ile	
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Arg Ser Leu Thr Lys Tyr Phe Leu Gln	Asp Ala Phe Gln Leu Arg	
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Tyr Leu Asp Leu Ser Ser Asn Lys Ile	Gln Met Ile Gln Lys Thr	
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Ser Phe Pro Glu Asn Val Leu Asn Asn	Leu Lys Met Leu Leu Leu	
770	775	780
His His Asn Arg Phe Leu Cys Thr Cys	Asp Ala Val Trp Phe Val	
785	790	795
Trp Trp Val Asn His Thr Glu Val Thr	Ile Pro Tyr Leu Ala Thr	
800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala	His Lys Gly Gln Ser Val	
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Ile Ser Leu Asp Leu Tyr Thr Cys Glu	Leu Asp Leu Thr Asn Leu	
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 <212> PRT
 <213> Homo sapiens

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 Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln Asn Asp Ser Val
 35 40 45
 Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr

				50					55					60
Val	Gly	Lys	Tyr	Val 65	Thr	Glu	Leu	Asp	Leu 70	Ser	Asp	Asn	Phe	Ile 75
Thr	His	Ile	Thr	Asn 80	Glu	Ser	Phe	Gln	Gly 85	Leu	Gln	Asn	Leu	Thr 90
Lys	Ile	Asn	Leu	Asn 95	His	Asn	Pro	Asn	Val 100	Gln	His	Gln	Asn	Gly 105
Asn	Pro	Gly	Ile	Gln 110	Ser	Asn	Gly	Leu	Asn 115	Ile	Thr	Asp	Gly	Ala 120
Phe	Leu	Asn	Leu	Lys 125	Asn	Leu	Arg	Glu	Leu 130	Leu	Leu	Glu	Asp	Asn 135
Gln	Leu	Pro	Gln	Ile 140	Pro	Ser	Gly	Leu	Pro 145	Glu	Ser	Leu	Thr	Glu 150
Leu	Ser	Leu	Ile	Gln 155	Asn	Asn	Ile	Tyr	Asn 160	Ile	Thr	Lys	Glu	Gly 165
Ile	Ser	Arg	Leu	Ile 170	Asn	Leu	Lys	Asn	Leu 175	Tyr	Leu	Ala	Trp	Asn 180
Cys	Tyr	Phe	Asn	Lys 185	Val	Cys	Glu	Lys	Thr 190	Asn	Ile	Glu	Asp	Gly 195
Val	Phe	Glu	Thr	Leu 200	Thr	Asn	Leu	Glu	Leu 205	Leu	Ser	Leu	Ser	Phe 210
Asn	Ser	Leu	Ser	His 215	Val	Pro	Pro	Lys	Leu 220	Pro	Ser	Ser	Leu	Arg 225
Lys	Leu	Phe	Leu	Ser 230	Asn	Thr	Gln	Ile	Lys 235	Tyr	Ile	Ser	Glu	Glu 240
Asp	Phe	Lys	Gly	Leu 245	Ile	Asn	Leu	Thr	Leu 250	Leu	Asp	Leu	Ser	Gly 255
Asn	Cys	Pro	Arg	Cys 260	Phe	Asn	Ala	Pro	Phe 265	Pro	Cys	Val	Pro	Cys 270
Asp	Gly	Gly	Ala	Ser 275	Ile	Asn	Ile	Asp	Arg 280	Phe	Ala	Phe	Gln	Asn 285
Leu	Thr	Gln	Leu	Arg 290	Tyr	Leu	Asn	Leu	Ser 295	Ser	Thr	Ser	Leu	Arg 300
Lys	Ile	Asn	Ala	Ala 305	Trp	Phe	Lys	Asn	Met 310	Pro	His	Leu	Lys	Val 315
Leu	Asp	Leu	Glu	Phe 320	Asn	Tyr	Leu	Val	Gly 325	Glu	Ile	Val	Ser	Gly 330
Ala	Phe	Leu	Thr	Met 335	Leu	Pro	Arg	Leu	Glu 340	Ile	Leu	Asp	Leu	Ser 345

Phe	Asn	Tyr	Ile	Lys	Gly	Ser	Tyr	Pro	Gln	His	Ile	Asn	Ile	Ser	350	355	360
Arg	Asn	Phe	Ser	Lys	Leu	Leu	Ser	Leu	Arg	Ala	Leu	His	Leu	Arg	365	370	375
Gly	Tyr	Val	Phe	Gln	Glu	Leu	Arg	Glu	Asp	Asp	Phe	Gln	Pro	Leu	380	385	390
Met	Gln	Leu	Pro	Asn	Leu	Ser	Thr	Ile	Asn	Leu	Gly	Ile	Asn	Phe	395	400	405
Ile	Lys	Gln	Ile	Asp	Phe	Lys	Leu	Phe	Gln	Asn	Phe	Ser	Asn	Leu	410	415	420
Glu	Ile	Ile	Tyr	Leu	Ser	Glu	Asn	Arg	Ile	Ser	Pro	Leu	Val	Lys	425	430	435
Asp	Thr	Arg	Gln	Ser	Tyr	Ala	Asn	Ser	Ser	Ser	Phe	Gln	Arg	His	440	445	450
Ile	Arg	Lys	Arg	Arg	Ser	Thr	Asp	Phe	Glu	Phe	Asp	Pro	His	Ser	455	460	465
Asn	Phe	Tyr	His	Phe	Thr	Arg	Pro	Leu	Ile	Lys	Pro	Gln	Cys	Ala	470	475	480
Ala	Tyr	Gly	Lys	Ala	Leu	Asp	Leu	Ser	Leu	Asn	Ser	Ile	Phe	Phe	485	490	495
Ile	Gly	Pro	Asn	Gln	Phe	Glu	Asn	Leu	Pro	Asp	Ile	Ala	Cys	Leu	500	505	510
Asn	Leu	Ser	Ala	Asn	Ser	Asn	Ala	Gln	Val	Leu	Ser	Gly	Thr	Glu	515	520	525
Phe	Ser	Ala	Ile	Pro	His	Val	Lys	Tyr	Leu	Asp	Leu	Thr	Asn	Asn	530	535	540
Arg	Leu	Asp	Phe	Asp	Asn	Ala	Ser	Ala	Leu	Thr	Glu	Leu	Ser	Asp	545	550	555
Leu	Glu	Val	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	His	Tyr	Phe	Arg	Ile	560	565	570
Ala	Gly	Val	Thr	His	His	Leu	Glu	Phe	Ile	Gln	Asn	Phe	Thr	Asn	575	580	585
Leu	Lys	Val	Leu	Asn	Leu	Ser	His	Asn	Asn	Ile	Tyr	Thr	Leu	Thr	590	595	600
Asp	Lys	Tyr	Asn	Leu	Glu	Ser	Lys	Ser	Leu	Val	Glu	Leu	Val	Phe	605	610	615
Ser	Gly	Asn	Arg	Leu	Asp	Ile	Leu	Trp	Asn	Asp	Asp	Asp	Asn	Arg	620	625	630
Tyr	Ile	Ser	Ile	Phe	Lys	Gly	Leu	Lys	Asn	Leu	Thr	Arg	Leu	Asp			

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Leu Ser Leu Asn Arg	Leu Lys His Ile	Pro Asn Glu Ala Phe	Leu		
	650		655		660
Asn Leu Pro Ala Ser	Leu Thr Glu Leu	His Ile Asn Asp Asn	Met		
	665		670		675
Leu Lys Phe Phe Asn	Trp Thr Leu Leu	Gln Gln Phe Pro Arg	Leu		
	680		685		690
Glu Leu Leu Asp Leu	Arg Gly Asn Lys	Leu Leu Phe Leu Thr	Asp		
	695		700		705
Ser Leu Ser Asp Phe	Thr Ser Ser Leu	Arg Thr Leu Leu Leu	Ser		
	710		715		720
His Asn Arg Ile Ser	His Leu Pro Ser	Gly Phe Leu Ser Glu	Val		
	725		730		735
Ser Ser Leu Lys His	Leu Asp Leu Ser	Ser Asn Leu Leu Lys	Thr		
	740		745		750
Ile Asn Lys Ser Ala	Leu Glu Thr Lys	Thr Thr Thr Lys Leu	Ser		
	755		760		765
Met Leu Glu Leu His	Gly Asn Pro Phe	Glu Cys Thr Cys Asp	Ile		
	770		775		780
Gly Asp Phe Arg Arg	Trp Met Asp Glu	His Leu Asn Val Lys	Ile		
	785		790		795
Pro Arg Leu Val Asp	Val Ile Cys Ala	Ser Pro Gly Asp Gln	Arg		
	800		805		810
Gly Lys Ser Ile Val	Ser Leu Glu Leu	Thr Thr Cys Val Ser	Asp		
	815		820		825
Val Thr Ala Val Ile	Leu Phe Phe Phe	Thr Phe Phe Ile Thr	Thr		
	830		835		840
Met Val Met Leu Ala	Ala Leu Ala His	His Leu Phe Tyr Trp	Asp		
	845		850		855
Val Trp Phe Ile Tyr	Asn Val Cys Leu	Ala Lys Val Lys Gly	Tyr		
	860		865		870
Arg Ser Leu Ser Thr	Ser Gln Thr Phe	Tyr Asp Ala Tyr Ile	Ser		
	875		880		885
Tyr Asp Thr Lys Asp	Ala Ser Val Thr	Asp Trp Val Ile Asn	Glu		
	890		895		900
Leu Arg Tyr His Leu	Glu Glu Ser Arg	Asp Lys Asn Val Leu	Leu		
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Cys Leu Glu Glu Arg	Asp Trp Asp Pro	Gly Leu Ala Ile Ile	Asp		
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 <223> Synthetic oligonucleotide probe

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<210> 504
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<212> PRT
<213> Homo sapiens

<400> 506
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Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	35	40	45
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	140	145	150
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	155	160	165
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	170	175	180
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	185	190	195
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	200	205	210
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	215	220	225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	230	235	240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	245	250	255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys	260	265	270
Lys	Asp	Ser															

<210> 507
 <211> 1700
 <212> DNA
 <213> Homo sapiens

<400> 507

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 gtgggccctc agctgaggga aggtacgagc tcctgctgg agcctgggac 1450
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<210> 510
 <211> 273
 <212> PRT
 <213> Homo sapiens

<400> 510
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 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
 35 40 45
 Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
 50 55 60
 Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
 65 70 75
 Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
 80 85 90
 Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
 95 100 105
 Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
 110 115 120
 Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
 125 130 135
 Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln

	140		145		150
Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu					
	155		160		165
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly					
	170		175		180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala					
	185		190		195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu					
	200		205		210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala					
	215		220		225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu					
	230		235		240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu					
	245		250		255
Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys					
	260		265		270
Lys Asp Ser					

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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 511
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<210> 512
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 512
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<210> 513
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 513
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<210> 514
 <211> 2690
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 2039-2065
 <223> unknown base

<400> 514
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 cccgctgggc cggtttatcg ggaggagatt gtcttcagg gctagcaatt 250
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<210> 515
 <211> 364
 <212> PRT
 <213> Homo sapiens

<400> 515
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 35 40 45
 Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu
 50 55 60
 Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu
 65 70 75
 Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp
 80 85 90
 Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile
 95 100 105
 Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln
 110 115 120
 Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile
 125 130 135
 Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro
 140 145 150
 Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe
 155 160 165
 Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn
 170 175 180
 Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr
 185 190 195
 Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser
 200 205 210
 Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr
 215 220 225
 Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val

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Gly Leu Thr Gly	Phe His Thr Phe Leu	Val Ala Leu Asn Gln Thr			
	245	250		255	
Thr Asn Glu Asp	Ile Lys Gly Ser Trp	Thr Gly Lys Asn Arg Val			
	260	265		270	
Gln Asn Pro Tyr	Ser His Gly Asn Ile	Val Lys Asn Cys Cys Glu			
	275	280		285	
Val Leu Cys Gly	Pro Leu Pro Pro Ser	Val Leu Asp Arg Arg Gly			
	290	295		300	
Ile Leu Pro Leu	Glu Glu Ser Gly Ser	Arg Pro Pro Ser Thr Gln			
	305	310		315	
Glu Thr Ser Ser	Ser Leu Leu Pro Gln	Ser Pro Ala Pro Thr Glu			
	320	325		330	
His Leu Asn Ser	Asn Glu Met Pro Glu	Asp Ser Ser Thr Pro Glu			
	335	340		345	
Glu Met Pro Pro	Pro Glu Pro Pro Glu	Pro Pro Gln Glu Ala Ala			
	350	355		360	
Glu Ala Glu Lys					

<210> 516
 <211> 255
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> unsure
 <222> 36, 38, 88, 118, 135, 193, 213, 222
 <223> unknown base

<400> 516
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 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200
 tcttcaccc ttttctctcc cncctcacia tctatgtctt cgccttcaac 250
 atcgt 255

<210> 517
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>

<223> Synthetic oligonucleotide probe

<400> 517

caacgtgatt tcaaagctgg gctc 24

<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtgaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

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<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150
 aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200
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aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600
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 aaacgtgaaa taaaaagagc aaaaaaaaaa 1679

<210> 523
 <211> 344
 <212> PRT
 <213> Homo sapiens

<400> 523

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				20					25					30	
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val	
				35					40					45	
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp	
				50					55					60	
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu	
				65					70					75	
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu	
				80					85					90	
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val	
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Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly	
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				155					160					165	
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val	
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Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln	
				185					190					195	
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro	
				200					205					210	
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile	
				215					220					225	
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr	

				230					235					240
Leu	Gln	Cys	Glu	Ala 245	Ser	Ala	Val	Pro	Ser 250	Ala	Glu	Phe	Gln	Trp 255
Tyr	Lys	Asp	Asp	Lys 260	Arg	Leu	Ile	Glu	Gly 265	Lys	Lys	Gly	Val	Lys 270
Val	Glu	Asn	Arg	Pro 275	Phe	Leu	Ser	Lys	Leu 280	Ile	Phe	Phe	Asn	Val 285
Ser	Glu	His	Asp	Tyr 290	Gly	Asn	Tyr	Thr	Cys 295	Val	Ala	Ser	Asn	Lys 300
Leu	Gly	His	Thr	Asn 305	Ala	Ser	Ile	Met	Leu 310	Phe	Gly	Pro	Gly	Ala 315
Val	Ser	Glu	Val	Ser 320	Asn	Gly	Thr	Ser	Arg 325	Arg	Ala	Gly	Cys	Val 330
Trp	Leu	Leu	Pro	Leu 335	Leu	Val	Leu	His	Leu 340	Leu	Leu	Lys	Phe	

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<210> 524
<211> 503
<212> DNA
<213> Homo sapiens
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cattgtgcaa gtatctccca aaattgtaga gatttcttca gatatctcca 450
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gag 503
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<210> 525
<211> 2602
<212> DNA
<213> Homo sapiens
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<400> 525
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Lys Lys Ser Cys	Val Pro Arg Trp Gln	Thr Cys Ile Ser Asn	Thr		
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Asp Asp Ala Leu	Gly Phe Ala Leu Gly	Ser Leu Phe Val Lys	Ala		
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Thr Phe Asp Arg	Gln Ser Lys Glu Ile	Ala Glu Gly Met Ile	Ser		
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Met Gly His Glu	Leu Thr His Ala Phe	Asp Asp Gln Gly Arg	Glu		
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Tyr Asp Lys Glu	Gly Asn Leu Arg Pro	Trp Trp Gln Asn Glu	Ser		
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 <211> 4308
 <212> DNA
 <213> Homo sapiens

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 <221> unsure
 <222> 1478, 3978, 4057-4058, 4070
 <223> unknown base

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<211> 1380

<212> DNA

<213> Homo sapiens

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<213> Artificial Sequence

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<210> 532
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<210> 533
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 <212> PRT
 <213> Homo Sapien

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 35 40 45
 Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu
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 Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile
 65 70 75
 Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser
 80 85 90
 Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn
 95 100 105
 Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr
 110 115 120
 Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln Val
 125 130 135
 Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu
 140 145 150
 Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu
 155 160 165
 Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe
 170 175 180
 Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln
 185 190 195
 Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro
 200 205 210
 Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile
 215 220 225
 Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu

Ile Arg Cys Glu Gly Ala Gly Val Pro	Pro Pro Ala Phe Glu Trp	230	235	240
	245	250	255	
Tyr Lys Gly Glu Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile	260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val	275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	320	325	330
Trp Tyr Leu Val Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr	335	340	345
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<211> 520

<212> PRT

<213> Homo Sapien

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			20					25						30

Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105
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Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135
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Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln	200	205	210
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln	215	220	225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys	230	235	240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro	245	250	255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met	260	265	270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro	275	280	285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln	290	295	300
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val	305	310	315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro			

320	325	330
Gly Arg Ala Gly Leu Pro Gly Ser Pro Gly Ser Pro Gly Ala Thr		
335	340	345
Gly Leu Lys Gly Ser Lys Gly Asp Thr Gly Leu Gln Gly Gln Gln		
350	355	360
Gly Arg Lys Gly Glu Ser Gly Val Pro Gly Pro Ala Gly Val Lys		
365	370	375
Gly Glu Gln Gly Ser Pro Gly Leu Ala Gly Pro Lys Gly Ala Pro		
380	385	390
Gly Gln Ala Gly Gln Lys Gly Asp Gln Gly Val Lys Gly Ser Ser		
395	400	405
Gly Glu Gln Gly Val Lys Gly Glu Lys Gly Glu Arg Gly Glu Asn		
410	415	420
Ser Val Ser Val Arg Ile Val Gly Ser Ser Asn Arg Gly Arg Ala		
425	430	435
Glu Val Tyr Tyr Ser Gly Thr Trp Gly Thr Ile Cys Asp Asp Glu		
440	445	450
Trp Gln Asn Ser Asp Ala Ile Val Phe Cys Arg Met Leu Gly Tyr		
455	460	465
Ser Lys Gly Arg Ala Leu Tyr Lys Val Gly Ala Gly Thr Gly Gln		
470	475	480
Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu		
485	490	495
Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His		
500	505	510
Glu Glu Asp Ala Gly Val Glu Cys Ser Val		
515	520	

<210> 615
 <211> 647
 <212> DNA
 <213> Homo Sapien

<400> 615
 cccacgcgtc cgaaggcaga caaaggttca tttgttaaaga agtccttcc 50
 agcacctcct ctcttctcct tttgcccaa ctcacccagt gagggtgagc 100
 atttaagaag catcctctgc caagaccaa aggaagaag aaaaagggcc 150
 aaaagccaaa atgaaactga tggacttgt tttcaccatt gggctaactt 200
 tgctgctagg agttcaagcc atgcctgcaa atgcctctc ttgctacaga 250
 aagatactaa aagatcacia ctgtcacaac cttccggaag gagtagctga 300

cctgacacag attgatgtca atgtccagga tcattttctgg gatgggaagg 350
 gatgtgagat gatctgttac tgcaacttca gccaattgct ctgctgcca 400
 aaagacgttt tctttggacc aaagatctct ttcgtgattc cttgcaacaa 450
 tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttccac 500
 aaactgcact acatcagtat aactgcattt ctagtttcta tatagtgcaa 550
 tagagcatag attctataaa ttcttacttg tctaagacaa gtaaactctgt 600
 gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaa 647

<210> 616
 <211> 98
 <212> PRT
 <213> Homo Sapien

<400> 616
 Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu
 1 5 10 15
 Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg
 20 25 30
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
 35 40 45
 Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp
 50 55 60
 Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu
 65 70 75
 Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser
 80 85 90
 Phe Val Ile Pro Cys Asn Asn Gln
 95

<210> 617
 <211> 2558
 <212> DNA
 <213> Homo Sapien

<400> 617
 cccacgcgtc cgcggacgcg tgggctggac cccaggtctg gagcgaattc 50
 cagcctgcag ggctgataag cgaggcatta gtgagattga gagagacttt 100
 accccgccgt ggtggttga gggcgcgcag tagagcagca gcacaggcgc 150
 ggggtcccggg aggccggctc tgctcgcgcc gagatgtgga atctccttca 200
 cgaaaccgac tcggctgtgg ccaccgcgcg ccgcccgcgc tggctgtgcg 250
 ctggggcgct ggtgctggcg ggtggcttct ttctcctcgg cttoctottc 300

ggggtgggtta taaaatcctc caatgaagct actaacatta ctccaaagca 350
 taatatgaaa gcatttttgg atgaattgaa agctgagaac atcaagaagt 400
 tcttacataa ttttacacag ataccacatt tagcaggaac agaacaaaac 450
 tttcagcttg caaagcaaatt tcaatcccag tggaaagaat ttggcctgga 500
 ttctgttgag ctagctcatt atgatgtcct gttgtcctac ccaaataaga 550
 ctcatcccaa ctacatctca ataattaatg aagatggaaa tgagattttc 600
 aacacatcat tatttgaacc acctcctcca ggatatgaaa atgtttcggg 650
 tattgtacca cttttcagtg ctttctctcc tcaaggaatg ccagagggcg 700
 atctagtgtg tggttaactat gcacgaactg aagacttctt taaattggaa 750
 cgggacatga aaatcaattg ctctgggaaa attgtaattg ccagatatgg 800
 gaaagttttc agaggaaata aggttaaaaa tgcccagctg gcagggggcca 850
 aaggagtcatt tctctactcc gaccctgctg actactttgc tcctgggggtg 900
 aagtcctatc cagacgggtg gaatcttctt ggaggtgggtg tccagcgtgg 950
 aaatatccta aatctgaatg gtgcaggaga ccctctcaca ccaggttacc 1000
 cagcaaatga atatgcttat aggcgtggaa ttgcagaggc tgttggtctt 1050
 ccaagtattc ctgttcatcc aattggatac tatgatgcac agaagctcct 1100
 agaaaaaatg ggtggctcag caccaccaga tagcagctgg agaggaagtc 1150
 tcaaagtgcc ctacaatgtt ggacctggct ttactggaaa cttttctaca 1200
 caaaaagtca agatgcacat ccactctacc aatgaagtga cgagaattta 1250
 caatgtgata ggtactctca gaggagcagt ggaaccagac agatatgtca 1300
 ttctgggagg tcacogggac tcatgggtgt ttggtggtat tgaccctcag 1350
 agtggagcag ctgttggtca tgaaattgtg aggagctttg gaacactgaa 1400
 aaaggaaggg tggagacctg gaagaacaat tttgtttgca agctgggatg 1450
 cagaagaatt tggctctctt ggttctactg agtgggcaga ggagaattca 1500
 agactccttc aagagcgtgg cgtggcttat attaagtctg actcatctat 1550
 agaaggaaac tacactctga gagttgattg tacaccgctg atgtacagct 1600
 tggtagacaa cctaacaaaa gagctgaaaa gccctgatga aggctttgaa 1650
 ggcaaattctc tttatgaaag ttggactaaa aaaagtcctt cccagagtt 1700
 cagtggcatg cccaggataa gcaaattggg atctggaaat gattttgagg 1750

tggttttcca acgacttga attgcttcag gcagagcacg gtataactaaa 1800
aattgggaaa caaacaatt cagcggctat ccactgtatc acagtgtcta 1850
tgaaacatat gagttggtgg aaaagtttta tgatccaatg tttaaatatc 1900
acctcactgt ggcccagggt cgaggagggg tgggtgttga gctagccaat 1950
tccatagtgc tcccttttga ttgtcgagat tatgctgtag ttttaagaaa 2000
gtatgctgac aaaatctaca gtatttctat gaaacatcca caggaaatga 2050
agacatacag tgtatcattt gattcacttt tttctgcagt aaagaatttt 2100
acagaaattg cttccaagtt cagtgcagaga ctccaggact ttgacaaaag 2150
caacccaata gtattaagaa tgatgaatga tcaactcatg tttctggaaa 2200
gagcatttat tgatccatta ggggtaccag acaggccttt ttataggcat 2250
gtcatctatg ctccaagcag ccacaacaag tatgcagggg agtcattccc 2300
aggaatttat gatgctctgt ttgatattga aagcaaagtg gacccttcca 2350
aggcctgggg agaagtgaag agacagattt atgttgcagc cttcacagtg 2400
caggcagctg cagagacttt gagtgaagta gcctaagagg attttttaga 2450
gaatccgtat tgaatttgtg tggatatgtc ctcagaaaga atcgtaatgg 2500
gtatattgat aaattttaaa attggtatat ttgaaataaa gttgaatatt 2550
atatataa 2558

<210> 618
<211> 750
<212> PRT
<213> Homo Sapien

<400> 618
Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala
1 5 10 15
Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly
20 25 30
Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser
35 40 45
Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
50 55 60
Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His
65 70 75
Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe
80 85 90

Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu
				95					100					105
Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro
				110					115					120
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly
				125					130					135
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly
				140					145					150
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser
				155					160					165
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala
				170					175					180
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn
				185					190					195
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg
				200					205					210
Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val
				215					220					225
Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys
				230					235					240
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg
				245					250					255
Gly	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro
				260					265					270
Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu
				275					280					285
Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr
				290					295					300
Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro
				305					310					315
Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly
				320					325					330
Pro	Gly	Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His
				335					340					345
Ile	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly
				350					355					360
Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly
				365					370					375
Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser

	380		385		390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr	Leu		
	395	400		405	
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala	Ser		
	410	415		420	
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp	Ala		
	425	430		435	
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr	Ile		
	440	445		450	
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val	Asp		
	455	460		465	
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys	Glu		
	470	475		480	
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr	Glu		
	485	490		495	
Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro		
	500	505		510	
Arg Ile Ser Lys	Leu Gly Ser Gly Asn	Asp Phe Glu Val Phe	Phe		
	515	520		525	
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys	Asn		
	530	535		540	
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser	Val		
	545	550		555	
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met	Phe		
	560	565		570	
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val	Phe		
	575	580		585	
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp	Tyr		
	590	595		600	
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile	Ser		
	605	610		615	
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Phe	Asp		
	620	625		630	
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser	Lys		
	635	640		645	
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile	Val		
	650	655		660	
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala	Phe		
	665	670		675	

Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	His	Val
				680					685					690
Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	Phe
				695					700					705
Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp
				710					715					720
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala
				725					730					735
Ala	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Ser	Glu	Val	Ala
				740					745					750

<210> 619
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 619
 agatgtgaag gtgcaggtgt gccg 24

<210> 620
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 620
 gaacatcagc gctcccggta attcc 25

<210> 621
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 621
 ccagcctttg aatggtacaa aggagagaag aagctcttca atggcc 46

<210> 622
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 622
 ccaaactcac ccagtgagtg tgagc 25

